

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 15:50:37 ; Search time 123 seconds

(without alignments)
399.701 Million cell updates/sec

Title: US-10-009-792C-19

Perfect score: 896

Sequence: 1 TPLGPASSLPQSFLKCLEQ.....SHLQSFLEVSVRLRLHAQP 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	896	100.0	174	1 AAP80965	Aap80965 G-CSF ded
2	896	100.0	174	1 AAP90470	Aap90470 G-colony
3	896	100.0	174	2 Aar13679	Aar13679 Granulocyte
4	896	100.0	174	2 Aar26909	Aar26909 Human G-C
5	896	100.0	174	2 Aar34707	Aar34707 Human CSF
6	896	100.0	174	2 Aar34707	Aar34707 Human G-C
7	896	100.0	174	3 AAY78937	Aay78937 Granulocyte
8	896	100.0	174	3 AAB14850	Aab14850 Human gra
9	896	100.0	174	3 AAY97016	Aay97016 Mature gr
10	896	100.0	174	4 AAE12153	Aae12153 Human hG-
11	896	100.0	174	4 AAB61930	Aab61930 Human gra
12	896	100.0	174	4 AAB55332	Aab55332 Codon opt
13	896	100.0	174	4 AAM52110	Aam52110 Human G-C
14	896	100.0	174	4 AAE11983	Aae11983 Human wil
15	896	100.0	174	5 AAU79877	Aau79877 Human gra
16	896	100.0	174	5 AAU97116	Aau97116 Wild-type
17	896	100.0	174	5 AAE14694	Aae14694 Human gra
18	896	100.0	174	6 ABR55839	Abr55839 Human gra
19	896	100.0	174	6 AAE30598	Aae30598 Human gra
20	896	100.0	174	6 ABG74368	Abg74368 Partial h
21	896	100.0	174	6 ABR62687	Abr62687 Human gra
22	896	100.0	174	7 ADC56722	Adc56722 Human pro
23	896	100.0	174	7 ABR61548	Abr61548 Human gra
24	896	100.0	174	7 ABR61549	Abr61549 Human gra
25	896	100.0	175	1 AAP71030	Aap71030 Sequence

26	896	100.0	175	1 AAP70732	Aap70732 Sequence
27	896	100.0	175	1 AAP90107	Aap90107 Human gra
28	896	100.0	175	1 AAP90170	Aap90170 Human gra
29	896	100.0	175	1 AAP91070	Aap91070 Human gra
30	896	100.0	175	2 AAR08486	Aar08486 Platelet
31	896	100.0	175	2 AAR98465	Aar98465 Human gra
32	896	100.0	175	2 AAW07533	Aaw07533 Recombina
33	896	100.0	175	2 AAR94394	Aar94394 PEGylated
34	896	100.0	175	2 AAW84297	Aaw84297 Human gra
35	896	100.0	175	3 AAY78936	Aay78936 Granulocyte
36	896	100.0	175	3 AAB14851	Aab14851 Human gra
37	896	100.0	175	3 AAY97017	Aay97017 Mature gr
38	896	100.0	175	3 AAB23758	Aab23758 Human gra
39	896	100.0	175	4 AAG67563	Aag67563 Amino aci
40	896	100.0	175	4 AAG67502	Aag67502 Amino aci
41	896	100.0	175	4 AAE12154	Aae12154 Human hG-
42	896	100.0	175	4 AAM52109	Aam52109 Human G-C
43	896	100.0	175	4 AAW51536	Aaw51536 Recombina
44	896	100.0	175	5 AAO19311	Aao19311 Branched
45	896	100.0	175	6 ABB97386	Abb97386 Recombina

ALIGNMENTS

RESULT 1

AAP80965
ID AAP80965 standard; protein; 174 AA.

XX AAP80965;

XX AC

XX 15-NOV-1990 (first entry)

XX DE G-CSF deduced from gene isolate from peripheral blood macrophages.

XX DE Granulocyte colony stimulating factor; hG-CSF; macrophage;

XX KW tumour therapy; leukaemia.

XX OS Homo sapiens.

XX PN EP272703-A.

XX PD 29-JUN-1988.

XX PF 23-DEC-1987; 87EP-00119157.

XX PR 23-DEC-1986; 86JP-00306799.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Kuga T, Komatsu Y, Miyaji H, Sato M, Okabe M, Morimoto M;

XX PI Itoh S, Yamasaki M;

XX DR WPI; 1988-176825/26.

XX DR N-PSDE; AAN80947.

XX FT Human granulocyte colony stimulating factor polypeptide derive. - having
XX PT at least one different aminoacid, giving high specific activity and
XX PT stability.
XX PS Disclosure; Page ?; 68pp; English.
XX CC The sequence of the gene is carried on plasmid pCSF1-2 isolated from a
XX CC cDNA library prepared from mRNA extracted from peripheral blood
XX CC macrophages. The deduced protein sequence agrees with those determined
XX CC for G-CSF from the human squamous cell line CHU-II and the human bladder
XX CC cancer cell line 5637. The DNA can be used as a "master gene" for the
XX CC construction of mutant genes which encode variants of hG-CSF which differ
XX CC by at least one AA. See also AAP80963 and AAP80964, and AAP82874-92
SQ Sequence 174 AA;

Query Match

100.0%; Score 896; DB 1; Length 174;

Best Local Similarity 100.0%; Pred. No. 3.8e-90; Mismatches 0; Indels 0; Gaps 0; Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60

QY 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 2
AAP90470
ID AAP90470 standard; protein; 174 AA.
XX AC AAP90470;
XX XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX DT
XX DE G-colony stimulating factor.
XX KW G-colony stimulating factor; G-CSF; lysine-depleted variant;
XX KW site-directed mutagenesis; human.
XX OS Homo sapiens.
XX OS
XX DN WO8905824-A.
XX PD
XX PD 29-JUN-1989.
XX PF
XX PF 22-DEC-1988; 88WO-US004633.
XX PR
XX PR 23-DEC-1987; 87US-00137043.
XX XX
XX PA (GEMY) GENETICS INST INC.
XX PI Shaw G;
XX PI
XX DR WPI; 1989-206594/28.
XX DR N-PSDB; AAN90256.
XX XX
XX FT New lysine depleted variants of polypeptide - opt. modified with
XX FT hydrophilic residues, biologically active but with altered solubility,
XX FT stability, etc.
XX PS
XX PS Disclosure; Fig 4; 35pp; English.
XX CC
XX CC DNA of G-CSF (G-colony stimulating factor) (see corresp. AAN90256). Used
XX CC in the patent to create lysine depleted variants by site-directed
XX CC mutagenesis, or synthesis. (Updated on 25-MAR-2003 to correct PA field.)
XX XX
SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-90; Mismatches 0; Indels 0; Gaps 0; Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60

QY 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 4
AAR26909
ID AAR26909 standard; protein; 174 AA.
XX AC AAR26909;
XX XX

Best Local Similarity 100.0%; Pred. No. 3.8e-90; Mismatches 0; Indels 0; Gaps 0; Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60

QY 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 3
AAR13679
ID AAR13679 standard; protein; 174 AA.
XX AC AAR13679;
XX XX
DT 25-MAR-2003 (revised)
DT 13-NOV-1991 (first entry)
XX DT
XX XX Granulocyte colony stimulating factor.
XX DE G-CSF; neutropaenia.
XX KW Synthetic.
XX OS
XX OS GB2241505-A.
XX PN
XX PD 04-SEP-1991.
XX XX
XX XX 27-FEB-1991; 91GB-00041260.
XX PF
XX PF 27-FEB-1990; 90GB-00004390.
XX PR
XX PR 27-FEB-1991; 91GB-00004126.
XX XX
XX XX (ICIL) IMPERIAL CHEM IND PLC.
XX PA
XX PA Hockney RC, Kara BV;
XX PI
XX PI WPI; 1991-262013/36.
XX DR N-PSDB; AAQ13329.
XX XX
XX FT Polypeptide prodn. by fermenting transformed host cells - in presence of
XX FT non-auxotrophic aminoacid to increase prod. accumulation, esp. for
XX FT granulocyte colony stimulating factor.
XX XX
XX PS Disclosure; Fig 6; 69pp; English.
XX CC
XX CC The protein was expressed from a synthetic gene designed to include
XX CC several restriction sites to facilitate manipulation and to have A/T rich
XX CC codons at the 5' end of the coding region. Other codons were chosen as
XX CC those preferred for expression in E. coli. The gene was cloned into an
XX CC expression plasmid for the prodn of G-CSF for use in the management of
XX CC neutropaenia etc. See also AAR14224. (Updated on 25-MAR-2003 to correct PR
XX CC field.) (Updated on 25-MAR-2003 to correct PA field.)
XX XX
SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-90; Mismatches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCPELVLLGHSGLGPWAP 60

QY 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 LSSCPSQALQACLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 4
AAR26909
ID AAR26909 standard; protein; 174 AA.
XX AC AAR26909;
XX XX

DT 25-MAR-2003 (revised)
 DT 20-MAY-1998 (first entry)
 XX Human G-CSF.
 DE
 XX G-CSF; granulocyte colony stimulating factor; inducible selection;
 KW ricin A; immunotoxins; neutropenia; chemotherapy; radiation; therapy;
 KW autologous bone marrow transplantation; AIDS; severe infection;
 KW myelodysplastic syndromes; abnormal granulocyte function.
 XX
 OS Synthetic.
 PN EP502637-A2.
 XX
 PD 09-SEP-1992.
 XX
 PF 21-FEB-1992; 92EP-00301465.
 XX
 PR 26-FEB-1991; 91GB-00004017.
 PR 29-APR-1991; 91GB-00009186.
 XX
 PA (ICIL) IMPERIAL CHEM IND PLC.
 PA (ZENE) ZENECA LTD.
 XX
 PI Barth PT;
 XX
 DR WPI; 1992-301941/37.
 DR N-PSDB; AAQ28371.
 XX
 XX Vector contg. inducible selection gene - encodes heterologous polypeptide
 PT e.g. ricin A and G-CSF.
 XX
 PS Claim 8; Fig 10; 73pp; English.
 XX
 CC This sequence is encoded by the synthetic gene AAQ28371. The plasmid
 CC containing the coding gene contains a novel inducible selection gene
 CC which is only expressed during the construction and testing phases of
 CC genetic manipulation. When the subsequent plasmid carrying the cloned
 CC gene is stably maintained in its bacterial host, the need for selection
 CC ceases. Cultures grown to express the cloned gene prod. will not require
 CC addn. of the selection drug and will not express the prod. of the
 CC selection gene. In this case the product of the cloned gene is human G-
 CC CSF which is used to treat neutropenia associated with chemotherapy,
 CC radiation therapy, or autologous bone marrow transplantation, to
 CC stimulate bone marrow suppression associated with AIDS, in the treatment
 CC of myelodysplastic syndromes characterised by granulocyte functional
 CC abnormalities and as an adjunct to the treatment of severe infections.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 174 AA;
 Query Match 100.0%; Score 896; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLLKCLQEVKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWAP 60
 DB 1 TPLGPASSLPQSFLLKCLQEVKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWAP 60
 QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 DB 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 QY 121 MEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 DB 121 MEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 QY 121 MEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 DB 121 MEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 RESULT 5
 AAR34707
 ID AAR34707 standard; protein; 174 AA.
 XX

AC AAR34707;
 XX 10-JUN-1993 (first entry)
 DT
 XX Human CSF analogue.
 DE
 XX Colony stimulating factor; cancer; tumour; sarcoma; lymphoma; melanoma;
 KW lung.
 KW
 OS Homo sapiens.
 PN JP05009131-A.
 XX
 PD 19-JAN-1993.
 XX
 PF 17-SEP-1991; 91JP-00236260.
 XX
 PR 17-SEP-1990; 90JP-00246488.
 PR 25-OCT-1990; 90JP-00287707.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 XX
 DR WPI; 1993-061608/08.
 XX
 XX Anticancer drug showing good apothanaisia effect - contains
 PT immuno-therapeutic agent for cancer, human colony stimulating factor and
 PT anticancer drug.
 XX
 PS Disclosure; Page 3; 10pp; Japanese.
 XX
 CC The sequence is that of human colony stimulating factor, which can be
 CC with an immunotherapeutic agent for cancer and an anticancer drug in a
 CC novel anticancer compsn. The compsn. has excellent anticancer effects,
 CC not shown by sole administration of the single components. It shows good
 CC life prolonging effects and has tumour growth inhibiting effects for
 CC mammalian cancers. It is esp. effective for treatment of early stage
 CC cancer and after cancer surgery. Treatable diseases include various kinds
 CC of sarcoma, malignant lymphoma, malignant melanoma, malignant chlorionic
 CC tumour, phalial cancer, various kinds of digestive organ cancer, lung
 CC cancer, etc. See also AAR32258
 XX
 SQ Sequence 174 AA;
 Query Match 100.0%; Score 896; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLLKCLQEVKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWAP 60
 DB 1 TPLGPASSLPQSFLLKCLQEVKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWAP 60
 QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 DB 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 QY 121 MEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 DB 121 MEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 RESULT 6
 AAW02204
 ID AAW02204 standard; protein; 174 AA.
 XX
 AC AAW02204;
 XX
 DT 10-OCT-1996 (first entry)
 XX
 XX Human G-CSF for stimulating peripheral blood cell prodn.
 DE
 KW Human; interleukin; hIL-11; granulocyte colony stimulating factor;
 KW hG-CSF; in vivo; increase; production; peripheral blood cells; hPBS;
 KW hIL-1; hIL-3; stem cell factor; leukaemia inhibitory factor;
 KW

KW erythropoietin; GM-CSF; M-CSF; transplant; treatment; transfusion;
 KW blood system disease.
 OS Homo sapiens.
 XX JP08127539-A.
 PN 21-MAY-1996.
 XX 31-OCT-1994; 94JP-00266826.
 XX 31-OCT-1994; 94JP-00266826.
 XX (AJIN) AJINOMOTO KK.
 PS WPI; 1996-295521/30.
 XX Agent contg. human interleukin 11 for increasing peripheral blood stem cell prodn. - pref. comprises human G-CSF, and is useful for peripheral blood stem cell transplants to treat blood system diseases.
 XX Example 1; Page 6; 6pp; Japanese.
 XX An agent contg. human interleukin 11 (hIL-11), and pref. human granulocyte colony stimulating factor (hG-CSF), i.e. the present protein, can be administered in vivo to increase the prodn. of human peripheral blood (hPES) cells. The agent may further comprise hIL-1, hIL-3, stem cell factor, leukemia inhibitory factor, erythropoietin, GM-CSF and M-CSF, which synergistically increase hPES cell prodn. . The amt. of hIL-11 or hIL-1 plus hG-CSF is generally 0.001-100, pref. 0.1-1.0 wt. %. The agent may contain a stabiliser (e.g. serum albumin) and fillers (mannitol). The dose is 0.1-1000 microg/kg/day, and the agent can be used in hPES cell transplants for the treatment of blood system diseases
 XX Sequence 174 AA;
 Query Match 100.0%; Score 896; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHPPELVLLGHSIGIPWAP 60
 Db 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHPPELVLLGHSIGIPWAP 60
 QY 61 LSSCPQALQALGCLSQLHSGLFLYQGLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 Db 61 LSSCPQALQALGCLSQLHSGLFLYQGLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
 Db 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
 RESULT 7
 AAY78937
 ID AAY78937 standard; protein; 174 AA.
 XX AAY78937;
 XX 05-JUN-2000 (first entry)
 XX Granulocyte colony-stimulation factor (G-CSF) peptide sequence #2.
 DE Granulocyte colony-stimulating factor; G-CSF; powder preparation;
 XX polymeric drug administration; mucus membranes.
 KW Homo sapiens.
 OS WO200002574-A1.
 PN 20-JAN-2000.
 XX 01-JUL-1999; 99WO-JP003563.
 PF

XX 08-JUL-1998; 98JP-00192722.
 PR 25-MAR-1999; 99JP-00081549.
 XX (KIRI) KIRIN ANGEM INC.
 XX Nomura H, Ueki Y;
 PI WPI; 2000-182173/16.
 DR Powder preparation for mucosal administration of polymeric drug, e.g. peptide, protein, antibody, vaccine or antigen.
 PT Disclosure; Page 39-40; 45pp; Japanese.
 PS This sequence represents a human granulocyte colony-stimulating factor (G-CSF) polypeptide. G-CSF is used in a powder preparation which is administered via the mucus membrane. The preparation comprises a polymeric medicine and a cationic polymer. The preparation is used for the mucosal administration of polymeric pharmaceuticals and has good absorption through the mucous membrane and improved bioavailability
 XX Sequence 174 AA;
 Query Match 100.0%; Score 896; DB 3; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHPPELVLLGHSIGIPWAP 60
 Db 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHPPELVLLGHSIGIPWAP 60
 QY 61 LSSCPQALQALGCLSQLHSGLFLYQGLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 Db 61 LSSCPQALQALGCLSQLHSGLFLYQGLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
 Db 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
 RESULT 8
 AAB14850
 ID AAB14850 standard; protein; 174 AA.
 XX AAB14850;
 XX 19-DEC-2000 (first entry)
 XX Human granulocyte colony stimulating factor #1.
 DE Human; granulocyte colony stimulating factor; G-CSF; neutropaenia;
 XX bone marrow suppression; infection.
 KW Homo sapiens.
 OS WO2000040728-A1.
 PN 13-JUL-2000.
 XX 06-JAN-2000; 2000WO-US000300.
 XX 06-JAN-1999; 99US-0115131P.
 PR 05-FEB-1999; 99US-0118831P.
 XX (XENC-) XENCOR INC.
 XX Dahiyat B, Luo P;
 PI WPI; 2000-465988/40.
 DR N-ESDB; AAA73324.
 XX A non-naturally occurring granulopoietic activity protein (GPA) for

PT treating granulocyte colony stimulating factor (G-CSF)-responsive disease
 PT comprises an amino acid sequence less than 95% identical to hG-CSF.

PS Disclosure; Fig 1; 63pp; English.

XX The present sequence is the protein sequence for the human granulocyte
 CC colony stimulating factor (G-CSF). This protein is involved in the
 CC proliferation and differentiation of granulocytes in the blood. The
 CC sequence was used to create the proteins of the invention, which are
 CC designated granulopoietic activity (GPA) proteins. These can be used
 CC instead of G-CSF, which has a short half-life in the blood and is
 CC unstable in storage, in treatments for neutropenia associated with
 CC cancer therapies, radiation accidents, bone marrow transplantation, bone
 CC marrow suppression conditions such as AIDS, myelodysplastic syndromes
 CC characterised by granulocyte functional abnormalities, and severe
 CC infections. They can also be used to enhance peripheral blood progenitor
 CC cell collection

XX Sequence 174 AA;

Query Match 100.0%; Score 896; DB 3; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
 DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
 QY 61 LSSCPQALQALGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWOQ 120
 DB 61 LSSCPQALQALGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWOQ 120
 QY 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 DB 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 9

AA97016
 ID AA97016 standard; protein; 174 AA.

AC AA97016;

DT 31-OCT-2000 (first entry)

DE Mature granulocyte colony stimulating factor.

KW G-CSF; granulocyte colony stimulating factor; sustained-release;
 KW biocompatible polyol/oil suspension; anti-inflammatory.

XX Homo sapiens.

XX WO200038652-A1.

XX 06-JUL-2000.

XX 20-DEC-1999; 99WO-US030527.

XX 23-DEC-1998; 98US-00221181.

XX 23-NOV-1999; 99US-00448205.

XX (AMGE-) AMGEN INC.

XX Goldenberg MS, Shan D, Beekman AC;

XX WPI; 2000-452289/39.

XX Pharmaceutical composition for the sustained-release of a biologically
 PT active agent (BAA), such as granulocyte-colony stimulating factor,
 PT comprises incorporating the BAA into a biocompatible polyol/oil
 PT suspension.

XX Claim 7; Page 11; 38pp; English.

XX A pharmaceutical composition comprising a biologically active agent (BAA)
 CC incorporated into a biocompatible polyol/oil suspension which contains a
 CC thickener is new. The compositions are used for the sustained-release of
 CC a BAA such as an interferon consensus, EPO, granulocyte-colony
 CC stimulating factor, stem cell factor, leptin, tumor necrosis factor-
 CC binding protein, interleukin-1 receptor antagonist, brain derived
 CC neurotrophic factor, glial derived neurotrophic factor, neutrophilic factor,
 CC 3, osteoprotegerin, granulocyte macrophage colony stimulating factor,
 CC megakaryocyte derived growth factor, keratinocyte growth factor,
 CC thrombopoietin, or novel erythropoiesis stimulating protein (claimed).
 CC The release of a medicament can be controlled to provide longer periods
 CC of consistent release that previous methods of treatment do not achieve,
 CC such as repeated injections. Blood levels of the active ingredient can be
 CC controlled, providing an enhanced prophylactic, therapeutic, or
 CC diagnostic effect as well as greater safety, patient convenience and
 CC patient compliance. The compositions can lead to dose sparing and a lower
 CC cost of protein production. Bioavailability and protein protection,
 CC stability and potency are increased

XX Sequence 174 AA;

Query Match 100.0%; Score 896; DB 3; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
 DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
 QY 61 LSSCPQALQALGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWOQ 120
 DB 61 LSSCPQALQALGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWOQ 120
 QY 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
 DB 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 10

AAE12153
 ID AAE12153 standard; protein; 174 AA.

AC AAE12153;

XX 18-DEC-2001 (first entry)

XX Human hG-CSF inserted into plasmid p19CSFm.

XX Human; granulocyte colony stimulating factor; hG-CSF; protease;
 XX Factor Xa; kanamycin resistance; endoxylanase signal peptide.

XX Homo sapiens.

XX WO200173081-A1.

XX 04-OCT-2001.

XX 31-MAR-2001; 2001WO-KR000549.

XX 31-MAR-2000; 2000KR-00017052.

XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.

XX Lee S, Jeong K;

XX WPI; 2001-616523/71.

XX N-PSDB; AAD19771.

XX Recombinant plasmid vector comprising an endoxylanase signal sequence,
 PT human granulocyte colony stimulating factor gene and other components,
 PT when transformed into microorganism useful for preparing the colony
 PT stimulating factor.

XX Example 1; Fig 3; 50pp; English.

XX The invention relates to an Escherichia coli producing and secreting

CC human granulocyte colony stimulating factor (hG-CSF), more specifically,

CC to a recombinant plasmid constructed to express secretory hG-CSF in E.

CC coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a

CC process for preparing hG-CSF using the transformed hG-CSF. The

CC recombinant plasmid vector comprises of a kanamycin resistance gene, a

CC promoter, an endoxylanase signal sequence, a nucleotide sequence coding

CC for an oligopeptide consisting of 13 amino acids including 6 consecutive

CC histidine residues and a hG-CSF. E.coli transformed with recombinant

CC plasmid vector is useful for preparing hG-CSF. The method comprises

CC culturing the microorganism to obtain a hG-CSF fusion protein and

CC treating the fusion protein with a protease preferably Factor Xa, to

CC obtain a hG-CSF, where the fusion protein is obtained from the culture by

CC employing Ni-column. The present sequence is human hG-CSF inserted into

CC plasmid p19CSFm

XX SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 4; Length 174;

Best Local Similarity 100.0%; Pred. No. 3.8e-90;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60

DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60

QY 61 LSSCPQALQALGCLSQLHSGFLYQGLQALLEGISPELGPTLDTLQLDVADPATTIWOQ 120

DB 61 LSSCPQALQALGCLSQLHSGFLYQGLQALLEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

DB 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 11

AAB61930

ID AAB61930 standard; protein; 174 AA.

XX AAB61930;

XX 08-MAY-2001 (first entry)

XX Human granulocyte-colony stimulating factor (hG-CSF).

XX Granulocyte-colony stimulating factor; G-CSF; human; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "can be replaced by Ser"

FT Misc-difference 2 /note= "can be replaced with met"

FT Misc-difference 3 /note= "can be replaced with Val"

FT Misc-difference 17 /note= "can be replaced with Ser, Thr, Ala or Gly"

XX WO200104329-A1.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-KR000733.

XX 08-JUL-1999; 99KR-00027418.

XX (HANM-) HANMI PHARM CO LTD.

XX Kwon SC, Jung SY, Bae SM, Lee GS;

XX WPI; 2001-138357/14.

DR N-PSDB; AAF56684.

XX Modified human granulocyte-colony stimulating factor (hG-CSF), retaining

PT the biological activity of wild type hG-CSF, comprises replacement amino

PT acids at the first, second, third and seventeenth positions.

XX Claim 1; Fig 1; 69pp; English.

XX The invention relates to a modified human granulocyte-colony stimulating

CC factor (hG-CSF), characterized in that at least one of the first, second,

CC third and seventeenth amino acids of wild-type hG-CSF (AAB61930) is

CC replaced by other amino acids. The modified hG-CSF retains the biological

CC activity of the wild-type protein. It does not have a methionine residue

CC at the N-terminus and so can be efficiently expressed and secreted by a

CC microorganism, when an appropriate secretory signal peptide is employed.

CC The modified hG-CSF is useful for processes requiring hG-CSF. The present

CC sequence represents the wild-type human hG-CSF mature protein

XX SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 4; Length 174;

Best Local Similarity 100.0%; Pred. No. 3.8e-90;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60

DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60

QY 61 LSSCPQALQALGCLSQLHSGFLYQGLQALLEGISPELGPTLDTLQLDVADPATTIWOQ 120

DB 61 LSSCPQALQALGCLSQLHSGFLYQGLQALLEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

DB 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 12

AAB85332

ID AAB85332 standard; protein; 174 AA.

XX AAB85332;

XX 17-SEP-2001 (first entry)

XX Codon optimised mature hG-CSF protein.

XX Granulocyte-colony stimulating factor; G-CSF; hemotopoietic; AIDS;

KW chemotherapy; immunodeficiency disease; anti-HIV; cytostatic;

KW antibacterial; gene therapy.

XX Homo sapiens.

XX WO200151510-A2.

XX 19-JUL-2001.

XX 09-JAN-2001; 2001WO-DK000011.

XX 10-JAN-2000; 2000DK-00000024.

XX 02-MAR-2000; 2000DK-00000341.

XX 16-JUN-2000; 2000DK-00000943.

XX (MAXY-) MAXYGEN APS.

XX Nissen TL, Andersen KV, Hansen CK, Mikkelsen JM, Schambye HT;

XX WPI; 2001-451839/48.

DR N-PSDB; AAH22902.

XX Novel polypeptides exhibiting granulocyte-colony stimulating factor

PT activity and conjugates between the polypeptide and a non-polypeptide
PT moiety, useful for treating leukopenia, AIDS and bacterial or other
PT infections.
XX
XX
PS Example 1; Page 91-92; 94pp; English.
XX
XX The invention provides a polypeptide (PP) conjugate (I) exhibiting
CC granulocyte-colony stimulating factor (G-CSF) activity, comprising PP
CC with an amino acid (aa) sequence that differs from aa sequence of human G
CC -CSF by at least one aa residue comprising an attachment group for a non-
CC PP group and having a non-PP group bound to attachment of PP, and the
CC polypeptide (II) portion of (I) exhibiting G-CSF activity. (I) and (II)
CC are useful for treating general hematopoietic disorders, including
CC disorders arising from radiation therapy or from chemotherapy, AIDS or
CC immunodeficiency diseases, leukopenia and bacterial or other infections.
CC (II) is useful for therapeutic, diagnostic and other purposes and in
CC particular finds use as intermediate products for preparation of (I). (I)
CC and (II) are used for preventing infection in cancer patients undergoing
CC radiation therapy, chemotherapy and bone marrow transplantations, to
CC mobilize progenitor cells for collection in peripheral blood progenitor
CC cell transplantations and to support treatment of patients with acute
CC myeloid leukemia. A nucleotide sequence encoding (II) is useful in gene
CC therapy applications. (I) has increased functional in vivo half-life,
CC increased serum half-life, reduced renal clearance, reduced receptor-
CC mediated clearance, reduced side effects, such as bone pain, reduced
CC immunogenicity and/or increased bioavailability. The present sequence
CC represents a mature hg-CSF with codon usage optimised for the encoding
CC DNA, for expression in *E. coli*. This is used in the construction of
CC synthetic genes encoding hg-CSF
XX
SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLHSLGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
QY 121 MEELGWAPALOPTQGAAPAFASAFORRAGGVIVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGWAPALOPTQGAAPAFASAFORRAGGVIVASHLQSFLEVSRYVLRHLAQP 174

RESULT 13
AAM52110
ID AAM52110 standard; protein; 174 AA.
XX
XX AAM52110;
AC AAM52110;
XX
DT 28-JAN-2002 (first entry)
XX
XX Human G-CSF polypeptide SEQ ID NO 2.
DE Human; G-CSF.
XX
XX Homo sapiens.
OS
XX WO200174397-A1.
FN
XX 11-OCT-2001.
PD
XX 28-MAR-2001; 2001WO-JP002555.
PF
XX 31-MAR-2000; 2000JP-00099213.
PR
XX (KIRI) KIRIN BEER KK.
PA
XX

PI Nomura H, Ueki Y;
XX
XX WPI; 2001-662952/76.
XX
XX Stable powdered preparation for transmemucosal administration comprises
XX polymeric drug, cationic polymer and basic amino acid.
PT
XX
XX Disclosure; Page 23-24; 28pp; Japanese.
PS
XX The invention relates to a stable powdered preparation for transmemucosal
XX administration (preferably nasally) comprising a polymeric form of drug
XX (preferably peptides), a cationic polymer and at least one basic amino
XX acid or its salt. The present sequence is that of human G-CSF polypeptide
XX
SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLHSLGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
QY 121 MEELGWAPALOPTQGAAPAFASAFORRAGGVIVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGWAPALOPTQGAAPAFASAFORRAGGVIVASHLQSFLEVSRYVLRHLAQP 174

RESULT 14
AAE11983
ID AAE11983 standard; protein; 174 AA.
XX
XX AAE11983;
AC
XX
DT 18-DEC-2001 (first entry)
XX
XX Human wild-type granulocyte colony stimulating factor (G-CSF).
DE
XX Human; interferon-gamma; IFNG; interferon-beta; interferon alpha; FSH;
KW follicle stimulating hormone; granulocyte colony stimulating factor;
KW G-CSF; interleukin 10; IL-10; medicament; pulmonary administration;
KW circulatory administration.
XX
XX Homo sapiens.
OS
XX WO200168141-A2.
FN
XX 20-SEP-2001.
PD
XX 16-MAR-2001; 2001WO-DK000182.
PF
XX 17-MAR-2000; 2000DK-00000447.
PR
XX 20-MAR-2000; 2000US-0190844P.
PR
XX 25-AUG-2000; 2000WO-DK000471.
PR
XX 13-NOV-2000; 2000WO-DK000631.
PR
XX (MAXY-) MAXYGEN APS.
PA
XX Hansen CK;
XX
XX WPI; 2001-616274/71.
FN
XX Dispersions of particles for administration to the lung and circulatory
XX system by inhalation, e.g. from a nebulizer.
PT
XX Claim 22; Page 138-139; 139pp; English.
PS
XX The present invention relates to novel dispersions of a conjugate
XX

CC comprising at least one non-polypeptide moiety covalently attached to a
 CC polypeptide variant, wherein the amino acid sequence of the polypeptide
 CC variant differs from that of the corresponding wild-type human
 CC polypeptide in that at least 1 residue comprising an attachment group for
 CC the non-polypeptide group has been introduced and/or removed. The wild-
 CC type human polypeptide is selected from the group consisting of
 CC interferon-gamma (IFNG), interferon-beta, interferon alpha, follicle
 CC stimulating hormone, (FSH), interleukin 10 (IL-10) and granulocyte colony
 CC stimulating factor (G-CSF). The dispersion is used for the preparation of
 CC a medicament for pulmonary and/or circulatory administration. The present
 CC sequence is human wild type granulocyte colony stimulating factor (G-CSF)
 XX
 XX
 SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 4; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLSGIPWAP 60
 DB 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLSGIPWAP 60
 QY 61 LSSCPSQALQALAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADFATTIQQ 120
 DB 61 LSSCPSQALQALAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADFATTIQQ 120
 QY 121 MEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYVLRHLAQP 174
 DB 121 MEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYVLRHLAQP 174

RESULT 15

AAU79877

ID AAU79877 standard; protein; 174 AA.

AC AAU79877;

15-JUL-2002 (first entry)

Human granulocyte colony-stimulating factor (G-CSF).

XX Human; granulocyte colony-stimulating factor; G-CSF; vasotropic;
 XX vunerary; immunosuppressive; cerebroprotective; nephrotropic;
 XX respiratory; cardiant; antiarteriosclerotic; ischaemic disease;
 XX external wound; transplant rejection; ischaemic cerebrovascular disorder;
 XX cerebral apoplexy; cerebral infarction; ischaemic kidney disease;
 XX ischaemic pulmonary disease; coronary occlusion; ischaemic limb disease;
 XX ischaemic heart disease; myocardial ischaemia; myocardial infarction;
 XX cardiac insufficiency; arteriosclerosis; kinesitherapy; pharmacotherapy;
 XX haemokinesis reconstruction; arteriosclerosis obliteran; gene therapy;
 XX intramuscular transplantation.

Homo sapiens.

WO200222163-A1.

21-MAR-2002.

13-SEP-2001; 2001WO-JP007946.

13-SEP-2000; 2000JP-00277562.

(CHUS) CHUGAI SEIYAKU KK.

Miyai T, Tamura M;

WPI; 2002-371949/40.

XX Remedies for ischemic diseases comprise human granulocyte colony-
 XX stimulating factor.

PS Disclosure; Page 4-5; 21pp; Japanese.

XX

CC The invention describes remedies comprising a human granulocyte colony-
 CC stimulating factor (G-CSF). Used for treating and preventing ischaemic
 CC diseases such as external wounds, transplant rejection, ischaemic
 CC cerebrovascular disorders (e.g. cerebral apoplexy and cerebral
 CC infarction), ischaemic kidney diseases, ischaemic pulmonary diseases,
 CC ischaemia due to coronary occlusion, ischaemic limb diseases, ischaemic
 CC heart disease (e.g. myocardial ischaemia, myocardial infarction or
 CC cardiac insufficiency) or arteriosclerosis. Agents may also be used for
 CC overcoming problems occurring particularly in the conventional
 CC kinesitherapy, pharmacotherapy and haemokinesis reconstruction for
 CC arteriosclerosis obliterans, gene therapy and intramuscular
 CC transplantation. This is the amino acid sequence of the human
 XX granulocyte colony-stimulating factor (G-CSF)
 XX
 SQ Sequence 174 AA;

Query Match 100.0%; Score 896; DB 5; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-90;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLSGIPWAP 60

DB 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLSGIPWAP 60

QY 61 LSSCPSQALQALAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADFATTIQQ 120

DB 61 LSSCPSQALQALAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADFATTIQQ 120

QY 121 MEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYVLRHLAQP 174

DB 121 MEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYVLRHLAQP 174

Search completed: October 6, 2004, 16:04:03

Job time : 129 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 16:02:01 ; Search time 32 Seconds
(without alignments)
280.716 Million cell updates/sec

Title: US-10-009-792C-19
Perfect score: 896
Sequence: 1 TPLGPASSLPQSFLKLCLEQ.....SHLQSFLEVSFVRLHQAQ 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pap.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pap.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pap.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	896	100.0	174	1	US-08-225-224-5
2	896	100.0	174	2	US-08-431-459A-31
3	896	100.0	174	3	US-08-722-258-5
4	896	100.0	174	3	US-09-221-181-1
5	896	100.0	174	4	US-09-904-196B-1
6	896	100.0	174	4	US-09-462-941-6
7	896	100.0	174	4	US-09-479-313B-2
8	896	100.0	174	4	US-09-760-008A-1
9	896	100.0	174	5	PCT-US95-04468-5
10	896	100.0	174	6	5194592-26
11	896	100.0	175	1	US-08-010-099-2
12	896	100.0	175	1	US-08-167-721-1
13	896	100.0	175	1	US-08-428-732-6
14	896	100.0	175	1	US-08-448-716-2
15	896	100.0	175	2	US-08-321-510-2
16	896	100.0	175	2	US-08-570-943-1
17	896	100.0	175	2	US-08-879-760-2
18	896	100.0	175	3	US-08-505-187-4
19	896	100.0	175	3	US-09-304-186-2
20	896	100.0	175	4	US-09-230-733-1
21	896	100.0	175	4	US-09-479-313B-15
22	896	100.0	175	4	US-09-754-532-2
23	896	100.0	175	5	PCT-US95-01729-2
24	896	100.0	176	3	US-08-469-318-161
25	896	100.0	176	3	US-08-468-609A-161
26	896	100.0	176	4	US-08-446-872A-161
27	896	100.0	176	4	US-08-762-227A-161

28	896	100.0	176	5	PCT-US95-01185-161	Sequence 161, App
29	896	100.0	177	2	US-08-797-689-14	Sequence 14, Appl
30	896	100.0	177	4	US-09-984-186-14	Sequence 14, Appl
31	896	100.0	204	1	US-08-792-019B-10	Sequence 10, Appl
32	896	100.0	204	3	US-08-988-819-10	Sequence 10, Appl
33	896	100.0	204	3	US-09-016-534-10	Sequence 10, Appl
34	896	100.0	204	3	US-08-097-869-5	Sequence 5, Appl
35	896	100.0	307	3	US-08-469-318-121	Sequence 121, App
36	896	100.0	307	3	US-08-469-318-134	Sequence 134, App
37	896	100.0	307	3	US-08-469-318-146	Sequence 146, App
38	896	100.0	307	3	US-08-469-318-147	Sequence 147, App
39	896	100.0	307	3	US-08-468-609A-121	Sequence 121, App
40	896	100.0	307	3	US-08-468-609A-134	Sequence 134, App
41	896	100.0	307	3	US-08-468-609A-146	Sequence 146, App
42	896	100.0	307	3	US-08-468-609A-147	Sequence 147, App
43	896	100.0	307	4	US-08-446-872A-131	Sequence 121, App
44	896	100.0	307	4	US-08-446-872A-134	Sequence 134, App
45	896	100.0	307	4	US-08-446-872A-146	Sequence 146, App

ALIGNMENTS

RESULT 1
US-08-225-224-5
; Sequence 5, Application US/08225224
; Patent No. 5635599
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: KREITMAN, Robert J.
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,224
; FILING DATE: 8-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..174
; OTHER INFORMATION: /label= G-CSF
US-08-225-224-5

Query Match 100.0%; Score 896; DB 1; Length 174;
Best Local Similarity 100.0%; Pred No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLGSLGIPWAP 60
Db 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLGSLGIPWAP 60
Qy 61 LSSCPQALQALQCLSQLSHGLFLYQGLLQALEGISPELGTDLTDLQDVADPATTIWOQ 120
Db 61 LSSCPQALQALQCLSQLSHGLFLYQGLLQALEGISPELGTDLTDLQDVADPATTIWOQ 120
Qy 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 2

US-08-431-459A-31
; Sequence 31, Application US/08431459A
; Patent No. 5840543
; GENERAL INFORMATION:
; APPLICANT: Hockney, Robert C.
; APPLICANT: Kara, Bhupendra V.
; TITLE OF INVENTION: FERMENTATION PROCESS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44M diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,459A
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,676
FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,306
FILING DATE: 27-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9004390.2
FILING DATE: 27-FEB-1990
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-431-459A-31

Query Match 100.0%; Score 896; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 4,3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLGSLGIPWAP 60
Db 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLGSLGIPWAP 60
Qy 61 LSSCPQALQALQCLSQLSHGLFLYQGLLQALEGISPELGTDLTDLQDVADPATTIWOQ 120
Db 61 LSSCPQALQALQCLSQLSHGLFLYQGLLQALEGISPELGTDLTDLQDVADPATTIWOQ 120
Qy 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 3

US-08-722-258-5

; Sequence 5, Application US/08722258
; Patent No. 601002
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Kreitman, Robert J.
; APPLICANT: Puri, Raj K.
; TITLE OF INVENTION: Circularly Permuted Ligands and
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..174
OTHER INFORMATION: /note= "granulocyte
US-08-722-258-5
OTHER INFORMATION: colony-stimulating factor (G-CSF)"

Query Match 100.0%; Score 896; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 4,3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLGSLGIPWAP 60
Db 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLGSLGIPWAP 60
Qy 61 LSSCPQALQALQCLSQLSHGLFLYQGLLQALEGISPELGTDLTDLQDVADPATTIWOQ 120
Db 61 LSSCPQALQALQCLSQLSHGLFLYQGLLQALEGISPELGTDLTDLQDVADPATTIWOQ 120
Qy 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 4

US-09-221-181-1

; Sequence 1, Application US/09221181

; Patent No. 6245740

GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, MERRILL
; APPLICANT: SHAN, DAXIAN
; APPLICANT: BREKMAN, ALICE
; TITLE OF INVENTION: POLYOL/OIL SUSPENSIONS FOR SUSTAINED RELEASE OF
; FILE REFERENCE: A-576
; CURRENT APPLICATION NUMBER: US/09/221,181
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: granulocyte colony-stimulating factor
US-09-221-181-1

Query Match 100.0%; Score 896; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 1 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 5
US-09-904-196B-1
; Sequence 1, Application US/09904,196B
; Patent No. 6555660
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAIVESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/904,196B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/760,008
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-196B-1

Query Match 100.0%; Score 896; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 6
US-09-462-941-6
; Sequence 6, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-6

Query Match 100.0%; Score 896; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPSQALQAGLSQHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 7
US-09-479-313B-2
; Sequence 2, Application US/09479313B
; Patent No. 6627186
; GENERAL INFORMATION:
; APPLICANT: Dahiya, Bassil I.
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEIN VARIANTS OF hG-CSF WITH GRANULOPOLYETIC
; FILE REFERENCE: A-67614-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/479,313B
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,131
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/118,831
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-479-313B-2

Query Match 100.0%; Score 896; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLHSLGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLHSLGIPWAP 60

QY 61 LSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGPTDLTDLQDVADPATTIQQ 120
DB 61 LSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGPTDLTDLQDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
DB 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174

RESULT 8

US-09-760-008A-1
; Sequence 1, Application US/09750008A
; Patent No. 6646110
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KASTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-00070005
; CURRENT APPLICATION NUMBER: US/09/760,008A
; PRIORITY FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-008A-1

Query Match 100.0%; Score 896; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLHSLGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLHSLGIPWAP 60

QY 61 LSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGPTDLTDLQDVADPATTIQQ 120
DB 61 LSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGPTDLTDLQDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
DB 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174

RESULT 9

PCT-US95-04468-5
; Sequence 5, Application PC/TUS9504468
; GENERAL INFORMATION:

APPLICANT: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
NUMBER OF SEQUENCES: 59
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468
FILING DATE: 07-APR-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-193-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..174
OTHER INFORMATION: /label= G-CSF
PCT-US95-04468-5

Query Match 100.0%; Score 896; DB 5; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLHSLGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPBEVLVLLHSLGIPWAP 60

QY 61 LSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGPTDLTDLQDVADPATTIQQ 120
DB 61 LSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGPTDLTDLQDVADPATTIQQ 120

QY 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
DB 121 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174

RESULT 10

5194592-26
; Patent No. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/318,527
FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 136,647
FILING DATE: 22-DEC-1987
; SEQ ID NO:26
; LENGTH: 174
5194592-26

Query Match 100.0%; Score 896; DB 6; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDVADFAATTIQQ 120
DB 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDVADFAATTIQQ 120
QY 121 MEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 11

US-08-010-099-2
; Sequence 2, Application US/08010099
; Patent No. 5591476
; GENERAL INFORMATION:
; APPLICANT: Otslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-010-099-2

Query Match 100.0%; Score 896; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 4.4e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
DB 2 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 61
QY 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDVADFAATTIQQ 120
DB 62 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDVADFAATTIQQ 121
QY 121 MEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 122 MEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 12

US-08-167-721-1
; Sequence 1, Application US/08167721

; Patent No. 5597562
; GENERAL INFORMATION:
; APPLICANT: No. 5597562ura, Hideaki
; APPLICANT: Maruyama, Kazutoshi
; TITLE OF INVENTION: Oral Dosage Form of Biologically Active
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marubai, O'Toole, Gerstein, Murray &
; ADDRESS: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,721
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,076
; FILING DATE:
; APPLICATION NUMBER: US/07/709,622
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Botun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 11009/30403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-167-721-1

Query Match 100.0%; Score 896; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 4.4e-92;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
DB 2 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 61
QY 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDVADFAATTIQQ 120
DB 62 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDVADFAATTIQQ 121
QY 121 MEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 122 MEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 13
US-08-428-732-6
; Sequence 6, Application US/08428732
; Patent No. 5606024
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Miller, Allan L.
; TITLE OF INVENTION: DNA Encoding Canine Granulocyte Colony
; TITLE OF INVENTION: Stimulating Factor (G-CSF)
; NUMBER OF SEQUENCES: 6


```

Db      2  TELGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSGLGPWAP 61
Qy      61  LSSCFPSOALQIAGCLSQLHSGFLYQGLLOALEGISPELGTDLTQLDQDVADPATTIWOQ 120
        |||||
Db      62  LSSCFPSOALQIAGCLSQLHSGFLYQGLLOALEGISPELGTDLTQLDQDVADPATTIWOQ 121
        |||||
Qy      121  MEELGNAPALOPTQGAMPAPAFASAFORRAGGVIVASHLOSFLVSVYRVLRLHAQP 174
        |||||
Db      122  MEELGNAPALOPTQGAMPAPAFASAFORRAGGVIVASHLOSFLVSVYRVLRLHAQP 175
        |||||

```

Search completed: October 6, 2004, 16:07:55
 Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 16:06:41 ; Search time 126 Seconds
(without alignments)
444.389 Million cell updates/sec

Title: US-10-009-792C-19

Perfect score: 896

Sequence: 1 TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEYSYRVLHQAQ 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	896	100.0	174	9	US-09-760-008A-1	Sequence 1, Appli
2	896	100.0	174	9	US-09-950-473-2	Sequence 2, Appli
3	896	100.0	174	9	US-09-921-114-1	Sequence 1, Appli
4	896	100.0	174	10	US-09-950-123-2	Sequence 2, Appli
5	896	100.0	174	12	US-10-411-037-2	Sequence 2, Appli
6	896	100.0	174	12	US-10-411-026-2	Sequence 2, Appli
7	896	100.0	174	12	US-10-467-396-1	Sequence 1, Appli
8	896	100.0	174	12	US-10-436-784-1	Sequence 1, Appli
9	896	100.0	174	13	US-10-016-403-1	Sequence 1, Appli
10	896	100.0	174	13	US-10-003-496-1	Sequence 1, Appli
11	896	100.0	174	14	US-10-192-294-1	Sequence 1, Appli
12	896	100.0	174	14	US-10-009-792A-19	Sequence 19, Appli
13	896	100.0	174	14	US-10-318-966-1	Sequence 1, Appli
14	896	100.0	174	14	US-10-400-377-6	Sequence 6, Appli
15	896	100.0	174	14	US-10-400-708-6	Sequence 6, Appli

16	896	100.0	174	14	US-10-298-148-6	Sequence 6, Appli
17	896	100.0	174	16	US-10-410-962-2	Sequence 2, Appli
18	896	100.0	174	16	US-10-411-049-2	Sequence 2, Appli
19	896	100.0	174	16	US-10-632-695-2	Sequence 2, Appli
20	896	100.0	174	16	US-10-930-2	Sequence 2, Appli
21	896	100.0	174	16	US-10-410-930-2	Sequence 2, Appli
22	896	100.0	174	16	US-10-411-012-2	Sequence 2, Appli
23	896	100.0	174	16	US-10-287-994-2	Sequence 2, Appli
24	896	100.0	174	16	US-10-410-913-2	Sequence 2, Appli
25	896	100.0	174	16	US-10-659-295-37	Sequence 37, Appli
26	896	100.0	174	16	US-10-750-797-1	Sequence 1, Appli
27	896	100.0	174	16	US-10-773-939-6	Sequence 6, Appli
28	896	100.0	174	16	US-10-774-149-6	Sequence 6, Appli
29	896	100.0	174	16	US-10-468-496-205	Sequence 205, App
30	896	100.0	175	9	US-09-754-532-2	Sequence 2, Appli
31	896	100.0	175	9	US-09-230-733-1	Sequence 1, Appli
32	896	100.0	175	9	US-09-921-114-2	Sequence 2, Appli
33	896	100.0	175	12	US-10-436-784-2	Sequence 2, Appli
34	896	100.0	175	12	US-09-817-725-2	Sequence 2, Appli
35	896	100.0	175	14	US-10-131-956-2	Sequence 2, Appli
36	896	100.0	175	14	US-10-264-846-2	Sequence 2, Appli
37	896	100.0	175	14	US-10-009-792A-21	Sequence 21, Appli
38	896	100.0	175	14	US-10-032-108-2	Sequence 2, Appli
39	896	100.0	175	14	US-10-345-639A-2	Sequence 2, Appli
40	896	100.0	175	14	US-10-365-418-1	Sequence 1, Appli
41	896	100.0	175	15	US-10-168-956A-3	Sequence 3, Appli
42	896	100.0	175	16	US-10-632-695-15	Sequence 15, Appli
43	896	100.0	175	16	US-10-659-295-38	Sequence 38, Appli
44	896	100.0	175	16	US-10-750-797-2	Sequence 2, Appli
45	896	100.0	176	14	US-10-083-446-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-09-760-008A-1
; Sequence 1, Application US/097600008A
; Patent No. US30020004483A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09760,008A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-008A-1

Query Match 100.0%; Score 896; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TELGPASSLPQSFLLKCLEQVNRKIQDGNALQEKLCATYKLPHELVLGHSLGPWAP 60

Db 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
QY 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 2

US-09-950-473-2
; Sequence 2, Application US/09950473
; Patent No. US20020151488A1
; GENERAL INFORMATION:
; APPLICANT: Sarkar, Casim
; APPLICANT: Lauferburger, Douglas
; TITLE OF INVENTION: G-CSF Analog Compositions and Methods
; FILE REFERENCE: 01017/37732
; CURRENT APPLICATION NUMBER: US/09/950,473
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-473-2

Query Match 100.0%; Score 896; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
Db 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
QY 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 3

US-09-921-114-1
; Sequence 1, Application US/09921114
; Patent No. US20020177688A1
; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/09/921,114
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620
; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-114-1

Query Match 100.0%; Score 896; DB 9; Length 174;

Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
Db 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
QY 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 4

US-09-950-123-2
; Sequence 2, Application US/09950123
; Publication No. US20030166527A1
; GENERAL INFORMATION:
; APPLICANT: Sarkar, Casim
; APPLICANT: Lauferburger, Douglas
; APPLICANT: Tidor, Bruce
; TITLE OF INVENTION: G-CSF Analog Compositions and Methods
; FILE REFERENCE: 01017/37377
; CURRENT APPLICATION NUMBER: US/09/950,123
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-123-2

Query Match 100.0%; Score 896; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
Db 1 TPLGPASSLPQSFLLKCLQEVKRIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAP 60
QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADPATTIWOQ 120
QY 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
Db 121 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 5

US-10-411-037-2
; Sequence 2, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692

Query Match 100.0%; Score 896; DB 10; Length 174;

```

; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-2

Query Match      100.0%; Score 896; DB 12; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLQEVVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
Db 1 TPLGPASSLPQSFLKCLQEVVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDVAADFATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDVAADFATTIWOQ 120

QY 121 MEELGNAPALQPTQGMPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
Db 121 MEELGNAPALQPTQGMPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174

RESULT 6
US-10-411-026-2
; Sequence 2, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-2

Query Match      100.0%; Score 896; DB 12; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLQEVVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
Db 1 TPLGPASSLPQSFLKCLQEVVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDVAADFATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDVAADFATTIWOQ 120

QY 121 MEELGNAPALQPTQGMPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
Db 121 MEELGNAPALQPTQGMPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174

RESULT 7
US-10-467-396-1
; Sequence 1, Application US/10467396
; Publication No. US20040062749A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED GRANULOCYTE COLONY STIMULATING
; TITLE OF INVENTION: FACTOR (G-CSF) WITH REDUCED IMMUNOGENICITY
; FILE REFERENCE: MER-113
; CURRENT APPLICATION NUMBER: US/10/467,396
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102617.6
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP/02/01171
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-396-1

Query Match      100.0%; Score 896; DB 12; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLQEVVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
Db 1 TPLGPASSLPQSFLKCLQEVVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDVAADFATTIWOQ 120
Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDVAADFATTIWOQ 120

QY 121 MEELGNAPALQPTQGMPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
Db 121 MEELGNAPALQPTQGMPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174

RESULT 8
US-10-436-784-1
; Sequence 1, Application US/10436784
; Publication No. US20030204057A1
; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/10/436,784
; CURRENT FILING DATE: 2003-05-12
```

us-10-009-792c-19.rapb

```
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620
; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-784-1

Query Match          100.0%; Score 896; DB 12; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAP 60

QY 61 LSSCPQALQALAGCISQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPQALQALAGCISQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGWAPALQPTQGMAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGWAPALQPTQGMAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 9
US-10-016-403-1
; Sequence 1, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
```

```
; LOCATION: 1..174
; OTHER INFORMATION: /note= "granulocyte-colony
; stimulating factor"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-016-403-1

Query Match          100.0%; Score 896; DB 13; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAP 60

QY 61 LSSCPQALQALAGCISQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPQALQALAGCISQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGWAPALQPTQGMAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGWAPALQPTQGMAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 10
US-10-003-496-1
; Sequence 1, Application US/10003496
; Publication No. US20020142964A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps
; TITLE OF INVENTION: Single-Chain Polypeptides
; FILE REFERENCE: 0218us210
; CURRENT APPLICATION NUMBER: US/10/003,496
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/245,727
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-496-1

Query Match          100.0%; Score 896; DB 13; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAP 60

QY 61 LSSCPQALQALAGCISQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120
DB 61 LSSCPQALQALAGCISQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWOQ 120

QY 121 MEELGWAPALQPTQGMAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
DB 121 MEELGWAPALQPTQGMAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 11
US-10-192-294-1
; Sequence 1, Application US/10192294
; Publication No. US20030118612A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, Torben Lauesgaard
; TITLE OF INVENTION: G-CSF Conjugates
; FILE REFERENCE: 0258us310
; CURRENT APPLICATION NUMBER: US/10/192,294
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 09/904,196
; PRIOR FILING DATE: 2001-07-11
```


; PRIOR APPLICATION NUMBER: DK PA 2002 00447
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: DK PA 2002 00708
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-192-294-1

Query Match 100.0%; Score 896; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPTLDTLQLDVADFTTIWQ 120
DB 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPTLDTLQLDVADFTTIWQ 120

QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 174
DB 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 174

RESULT 12
US-10-009-792A-19
; Sequence 19, Application US/10009792A
; Publication No. US20030153049A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; APPLICANT: JEONG, Ki-Jun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; FILE REFERENCE: HYLEE60.001APC
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-009-792A-19

Query Match 100.0%; Score 896; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPTLDTLQLDVADFTTIWQ 120
DB 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPTLDTLQLDVADFTTIWQ 120

QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 174
DB 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 174

RESULT 13
US-10-318-966-1
; Sequence 1, Application US/10318966

; Publication No. US20030158375A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; APPLICANT: SCHAMBYE, HANS THALSIGARD
; TITLE OF INVENTION: G-CSF POLYPEPTIDES AND CONJUGATES
; FILE REFERENCE: 0208us620
; CURRENT APPLICATION NUMBER: US/10/318,966
; CURRENT FILING DATE: 2002-12-13
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/904,196
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-966-1

Query Match 100.0%; Score 896; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60

QY 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPTLDTLQLDVADFTTIWQ 120
DB 61 LSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPTLDTLQLDVADFTTIWQ 120

QY 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 174
DB 121 MEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 174

RESULT 14
US-10-400-377-6
; Sequence 6, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: COX III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-400-377-6

	Query Match	100.0%;	Score 896;	DB 14;	Length 174;
	Best Local Similarity	100.0%;	Pred. No. 2.3e-85;		
	Matches 174;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TPLPGASLPOSFLKCLEQVRKIQDGAALQEKLCATYKLCPSBELVLGHSIGIPWAP	60		
Db	1	TPLPGASLPOSFLKCLEQVRKIQDGAALQEKLCATYKLCPSBELVLGHSIGIPWAP	60		
Qy	61	LSSCPSQALQAGCLSQHSGFLFYQGLLQALEGISPELGPTLDTQLQDVADFATTWQQ	120		
Db	61	LSSCPSQALQAGCLSQHSGFLFYQGLLQALEGISPELGPTLDTQLQDVADFATTWQQ	120		
Qy	121	MEELGMAPALOPTGAMPATASAFORRAGCVLVASHLQSFLEVSRYVLRHLHAQP	174		
Db	121	MEELGMAPALOPTGAMPATASAFORRAGCVLVASHLQSFLEVSRYVLRHLHAQP	174		

RESULT 15

```

RESUL 15
US-10-400-708-6
; Sequence 6, Application US/10400708
; Publication No. US2003016865A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-6

```

	Query Match	100.0%;	Score 896;	DB 14;	Length 174;
	Best Local Similarity	100.0%;	Pred. No. 2.3e-85;		
	Matches 174;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TPLPASLSLPOSFLKCLEQVRKIOGDGAALQEKICATYKLCHEPELVLLGHSLGIPWAP	60		
Db	1	TPLPASLSLPOSFLKCLEQVRKIOGDGAALQEKICATYKLCHEPELVLLGHSLGIPWAP	60		
QY	61	LSSCPSQALQAGCLSQLHSGFLYQGLLQALQEGISPELGPPTDLTQLQDVADPATTWQQ	120		
Db	61	LSSCPSQALQAGCLSQLHSGFLYQGLLQALQEGISPELGPPTDLTQLQDVADPATTWQQ	120		
QY	121	NEELGMAPALQPTQCAMPAFAFAFORRAGCVLVASHLOSFLEVSRYVRHLHAQP	174		
Db	121	NEELGMAPALQPTQCAMPAFAFAFORRAGCVLVASHLOSFLEVSRYVRHLHAQP	174		

Search completed: October 6, 2004, 16:18:30
Job time : 128 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 15:59:42 ; Search time 39 Seconds

(without alignments)
429.162 Million cell updates/sec

Title: US-10-009-792C-19

Perfect score: 896

Sequence: 1 TPLGPASLSLQSFLLKCLEQ.....SHLQSFLEVSRYVLRHLAQP 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	896	100.0	204	1 F0HUGL	granulocyte colony
2	884.5	98.7	207	2 A24573	granulocyte colony
3	744	83.0	194	2 T09255	granulocyte colony
4	738	82.4	174	2 T10268	granulocyte colony
5	641	71.5	208	2 A26496	granulocyte colony
6	634	70.8	214	2 J05043	granulocyte colony
7	304	33.9	201	2 A42247	myelomonocytic gro
8	106.5	11.9	212	2 I46621	prointerleukin 6 -
9	106.5	11.9	212	2 I46590	interleukin 6 - pi
10	100	11.2	208	2 T09216	interleukin-6 prec
11	94	10.5	345	2 C82270	hypothetical prote
12	89.5	10.0	2175	1 S03170	homeotic protein c
13	88.5	9.9	666	2 A87577	oligopeptide trans
14	88.5	9.9	786	2 F83292	probable sensor/re
15	86	9.6	208	1 A36610	interleukin-6 prec
16	86	9.6	502	2 S46506	H+-transporting tw
17	85	9.5	207	2 I46084	interleukin 6 - ca
18	84	9.4	274	1 C93362	conserved hypothet
19	83.5	9.3	846	2 J07721	aryl hydrocarbon r
20	80.5	9.0	406	2 B72766	probable threonyl-
21	80	8.9	474	2 D75550	probable D-alanyl-
22	80	8.9	477	2 T46304	hypothetical prote
23	79.5	8.9	351	2 T19623	hypothetical prote
24	79	8.8	423	2 AC3553	4-aminobutyrate tr
25	78	8.7	208	1 S29549	interleukin-6 - sh
26	78	8.7	316	2 H82958	homoserine kinase
27	77.5	8.6	653	2 C82580	oligopeptide trans
28	77	8.6	974	2 AC2076	two-component hybr
29	76.5	8.5	195	2 JH0680	ciliary neurotroph

RESULT 1

F0HUGL

granulocyte colony-stimulating factor precursor - human

N;Alternate names: colony-stimulating factor 3; G-CSF

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 22-Jun-1999

C;Accession: A25093; A49796; A47587; S68331

R;Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.;

EMBO J. 5, 575-581, 1986

A;Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stim

A;Reference number: A25093; MUID:86220137; PMID:2423327

A;Accession: A25093

A;Molecule type: DNA; mRNA

A;Residues: 1-204 <NAG>

A;Cross-references: EMBL:X03656; EMBL:X03655; NID:G31693; PIDN:CAA27290.1; PID:9732764

J. Leukoc. Biol. 41, 302-306, 1987

R;Devlin, J.C.; Devlin, P.B.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.

A;Title: Expression of granulocyte colony-stimulating factor by human cell lines.

A;Reference number: A49796; MUID:87196936; PMID:3494801

A;Accession: A49796

A;Molecule type: mRNA

A;Residues: 1-204 <DEV>

A;Cross-references: GB:M17706; NID:G183040; PIDN:AAA35882.1; PID:G183041

R;Souza, L.M.; Boons, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Murdock, D.C.; Chazi;

Science 232, 61-65, 1986

A;Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and

A;Reference number: A47587; MUID:86151684; PMID:2420009

A;Accession: A47587

A;Molecule type: mRNA

A;Residues: 19-204 <SOU>

A;Cross-references: GB:M13008; NID:G183044; PIDN:AAA03056.1; PID:G183045

R;Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.

Arch. Biochem. Biophys. 324, 344-356, 1995

A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.

A;Reference number: S68331; MUID:96132662; PMID:8554326

A;Accession: S68331

A;Molecule type: protein

A;Residues: 'M'/31-46 <HAN>

C;Genetics:

A;Gene: GDB:CSF3

A;Cross-references: GDB:115083; OMIM:138970

A;Map position: 17q11.2-17q12

A;Introns: 14/1; 65/3; 101/3; 150/3

C;Function:

A;Description: stimulates the differentiation and proliferation of hematopoietic progen.

C;Superfamily: interleukin-6

C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-204/Product: granulocyte colony-stimulating factor #status predicted <WAT>

F;66-72,94-104/Disulfide bonds: #status predicted

Query Match 100.0%; Score 896; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 7.8e-78; Indels 0; Gaps 0;
 Matches 174; Conservative 0; Mismatches 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIPWAP 60
 DB 31 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIPWAP 90
 QY 61 LSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTIWOQ 120
 DB 91 LSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTIWOQ 150
 QY 121 MEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 174
 DB 151 MEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 204

RESULT 2
 A24573
 granulocyte colony-stimulating factor precursor variant splice form CHU-2 - human
 N;Alternate names: colony-stimulating factor 3; G-CSF
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
 C;Accession: A24573
 R;Ragata, S.; Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Y.
 Nature 319, 415-418, 1986
 A;Title: Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor
 A;Reference number: A24573; MUID:86118679; PMID:3484805
 A;Accession: A24573
 A;Molecule type: mRNA
 A;Residues: 1-207 <NAG>
 A;Cross-references: EMBL:X03438; NID:g31689; PIDN:CAA27168.1; PID:g31690
 C;Comment: This variant splice form is not expressed in three other cell lines and may be
 C;Genetics:
 A;Gene: GDB:CSF3
 A;Cross-references: GDB:119083; OMIM:138970
 A;Map position: 17q11.2-17q12
 A;Introns: 14/1; 68/3; 104/3; 153/3
 C;Superfamily: interleukin-6
 C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-207/Product: granulocyte colony-stimulating factor variant splice form CHU-2 #status
 F;69-75,97-107/Disulfide bonds: #status predicted

Query Match 98.7%; Score 884.5; DB 2; Length 207;
 Best Local Similarity 98.3%; Pred. No. 9.9e-77; Indels 3; Gaps 1;
 Matches 174; Conservative 0; Mismatches 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIP 57
 DB 31 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLVSECATYKLCHEPVLVLLGHSIGIP 90
 QY 58 WAPLSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTI 117
 DB 91 WAPLSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTI 150
 QY 118 WQMEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 174
 DB 151 WQMEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 207

RESULT 3
 T09255
 granulocyte colony-stimulating factor precursor - cat (fragment)
 C;Species: Felis silvestris catus (domestic cat)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
 C;Accession: T09255
 R;Dunham, S.P.; Ontons, D.E.
 submitted to the EMBL Data Library, September 1996
 A;Description: Cloning, sequence and expression of feline granulocyte colony stimulating
 A;Reference number: Z16630
 A;Accession: T09255
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-194 <DUN>
 A;Cross-references: EMBL:Y08558
 C;Function:
 A;Description: stimulates the differentiation and proliferation of hematopoietic progenitor
 C;Superfamily: interleukin-6
 C;Keywords: cytokine; growth factor; macrophage
 F;1-20/Domain: signal sequence (fragment) #status predicted <SIG>
 F;21-194/Product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match 83.0%; Score 744; DB 2; Length 194;
 Best Local Similarity 81.0%; Pred. No. 2.1e-63; Indels 0; Gaps 0;
 Matches 141; Conservative 11; Mismatches 22;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIPWAP 60
 DB 21 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIPWAP 80
 QY 61 LSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTIWOQ 120
 DB 81 LSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTIWOQ 140
 QY 121 MEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 174
 DB 141 MEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 194

RESULT 4
 T10268
 granulocyte colony-stimulating factor - sheep (fragment)
 C;Species: Ovis orientalis aries. Ovis ammon aries (domestic sheep)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T10268
 R;O'Brien, P.M.; Secow, H.F.; Rotheil, J.S.; Wood, P.R.
 DNA Seq. 4, 339-342, 1994
 A;Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDNA.
 A;Reference number: Z17009; MUID:95102116; PMID:7528579
 A;Accession: T10268
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-174 <OR>
 A;Cross-references: EMBL:L07939; NID:g310381; PIDN:AAA68006.1; PID:g310382
 C;Genetics:
 A;Gene: CSF
 C;Function:
 A;Description: stimulates the differentiation and proliferation of hematopoietic progenitor
 C;Superfamily: interleukin-6
 C;Keywords: cytokine; growth factor; macrophage

Query Match 82.4%; Score 738; DB 2; Length 174;
 Best Local Similarity 82.2%; Pred. No. 6.9e-63; Indels 0; Gaps 0;
 Matches 143; Conservative 10; Mismatches 21;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIPWAP 60
 DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPVLVLLGHSIGIPWAP 60
 QY 61 LSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTIWOQ 120
 DB 61 LSSCPSQALQALQCLSQLHSGFLYQGLLQALLEGISPELGPDLTDLQDVADPATTIWOQ 120
 QY 121 MEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 174
 DB 121 MEELGNAPALQPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLHAQP 174

RESULT 5
 A26496
 granulocyte colony-stimulating factor precursor - mouse
 N;Alternate names: G-CSF
 C;Species: Mus musculus (house mouse)
 C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 16-Jul-1999
 C;Accession: A29536; A26496; S02493

R,Tsuchiya, M.; Kaziro, Y.; Nagata, S.
Eur. J. Biochem. 165, 7-12, 1987
A:Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor
A:Reference number: A29536; MUID:87190474; PMID:3494605
A:Accession: A29536
A:Molecule type: DNA
A:Residues: 1-208 <TS>
A:Cross-references: GB:X05402; NID:G51059; PIDN:CA28986.1; PID:G51060
R,Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986
A:Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor.
A:Reference number: A26496; MUID:87017003; PMID:3489940
A:Accession: A26496
A:Molecule type: mRNA
A:Residues: 1-208 <TS>
A:Cross-references: GB:M13926; NID:G193451; PIDN:AAA37672.1; PID:G309248
R,Simpson, R.J.; Nice, E.C.; Nicola, N.A.
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987
A:Title: Structural studies on the murine granulocyte colony-stimulating factor.
A:Reference number: S02493; MUID:88106998; PMID:3501294
A:Accession: S02493
A:Status: preliminary
A:Molecule type: protein
A:Residues: 31-34, 'X', '36-43; 48-51, 'X', '53-57; 'X', '60-71; 159-164, 'X', '166-176; 183-198, 'X', '200-203
C:Genetics:
A:Introns: 14/1; 71/3; 107/3; 156/3
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor; macrophage; monomer

Query Match 71.5%; Score 641; DB 2; Length 208;
Best Local Similarity 75.9%; Pred. No. 1.4e-53;
Matches 129; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

QY 3 LGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGSHLGPWPAPLS 62
Db LPSPPLPRSPFLKLEQVRKIQAGSVLLQCLCATYKLCHEPELVLLGSHLGPKASLS 98

QY 63 SCPSQALQAGCLSLHSGFLYQGLQALEGISPELQPTLDTLQLDVADPATTIWOQME 122
Db GCSSQALQQTCLSLHSGFLYQGLQALSISPALAPTLLDQLDVAPEATTIWOQME 158

QY 123 ELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSRYVRHLA 172
Db NLGVAPTQPTQSTAMPATSAFORRAGGVVLAISLQGFLETARLALHHLA 208

RESULT 6
JC5043
granulocyte colony-stimulating factor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 16-Jul-1999
C:Accession: JC5043
R:Han, S.W.; Ramesh, N.; Osborne, W.R.A.
Gene 175, 101-104, 1995
A:Title: Cloning and expression of the cDNA encoding rat granulocyte colony-stimulating factor.
A:Reference number: JC5043; MUID:197074656; PMID:8917083
A:Accession: JC5043
A:Molecule type: mRNA
A:Residues: 1-214 <HAN>
A:Cross-references: GB:U37101; NID:G1680658; PIDN:AAC52915.1; PID:G1680659
A:Experimental source: skin fibroblasts
C:Comment: This receptor acts on precursor hemopoietic cells to control the production of interleukin-6
C:Superfamily: interleukin-6
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-214/Product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match 70.8%; Score 634; DB 2; Length 214;
Best Local Similarity 73.8%; Pred. No. 6.9e-53;
Matches 127; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 3 LGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGSHLGPWPAPLS 62
Db LPSPPLPRSPFLKLEQVRKIQARNTLEQLCATYKLCHEPELVLLGSHLGPKASLS 89

QY 63 SCPSQALQAGCLSLHSGFLYQGLQALEGISPELQPTLDTLQLDVADPATTIWOQME 122
Db SCSSQALQQTCLSLHSGFLYQGLQALAGISSELATPLDMLHLDVDPATTIWOQME 149

QY 123 ELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSRYVRHLAQP 174
Db SLGVAPTQPTQSTAMPATSAFORRAGGVVTSYLQSFLETAAHHLHLPRP 201

RESULT 7
A42247
myelomonocytic growth factor precursor - chicken
N:Alternate names: colony-stimulating factor cMGF
C:Species: Gallus gallus (Chicken)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A42247; S03633
R:Sternbeck, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A:Title: Structure of the chicken myelomonocytic growth factor gene and specific activation of the chicken myelomonocytic growth factor (cMGF) reveals a novel growth factor.
A:Reference number: A42247; MUID:92195319; PMID:1549124
A:Accession: A42247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <STE>
A:Note: sequence extracted from NCBI backbone (NCBI:89832, NCBI:89836)
R:Leutz, A.; Damm, K.; Sternbeck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Paembo, J.
EMBO J. 8, 175-181, 1989
A:Title: Molecular cloning of the chicken myelomonocytic growth factor (cMGF) reveals a novel growth factor.
A:Reference number: S03633; MUID:89231616; PMID:2785450
A:Accession: S03633
A:Molecule type: mRNA
A:Residues: 1-201 <LEU>
A:Cross-references: EMBL:X14477; NID:G63396; PIDN:CAA32639.1; PID:G63597
C:Superfamily: interleukin-6
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-201/Product: myelomonocytic growth factor #status predicted <MAT>
F:123,137/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.9%; Score 304; DB 2; Length 201;
Best Local Similarity 40.6%; Pred. No. 1.6e-21;
Matches 67; Conservative 28; Mismatches 68; Indels 2; Gaps 1;

QY 11 QSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGSHLGPWPAPLSQALQ 70
Db QLFELKMLETRKIRGDAALQRAVCDTFLQCTEELQVLQPPHVLQAPLDQCHKRGFQ 95

QY 71 LAGCLSLHSGFLYQGLQALEGISPELQPTLDTLQLDVADPATTIWOQMEELGMAPAL 130
Db AEVCFQIRAGLHAYHDSLCVLRLLPNHTLTVETLQDAANLSSNIQQOMEDLGLDVT 155

QY 131 QPTQ--GAMPAPAFASAFORRAGGVVASHLQSFLEVSRYVRHLAQP 173
Db LPAPQSPPTFGPQQVGGFFILANFORFLETATRALHLAR 200

RESULT 8
146621
prointerleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146621
R:Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of Interleukin 6
A:Reference number: 146621; MUID:91338547; PMID:1873476
A:Accession: 146621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RC>
A:Cross-references: GB:M86722; NID:G164624; PIDN:AAC37333.1; PID:G164625
C:Genetics:

A:Gene: IL6
C:Superfamily: interleukin-6

Query Match 11.9%; Score 106.5; DB 2; Length 212;
Best Local Similarity 22.6%; Pred. No. 0.01;
Matches 36; Conservative 33; Mismatches 85; Indels 5; Gaps 3;
QY 16 KCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIP-WAPLSSCPQALQAGC 74
DB 52 KTEELIKYLGKTSAMRKEMCEKYEKENSKEVLAENNLNPKMAEKDGCFOGFGNQETC 111
QY 75 LSQHLGSLFLYQGLQALGEGISPELGPTLDTLQLDVADPATTIWOQMEELGNAPALQPT- 133
DB 112 LMRITGLVEFQIYLDYLOKEVESNKGNGVEAQVISTKALIQTLRQKGNPKATTPNPTT 171
QY 134 -QGAMPAPAS--AFQRRAGGVLVASHLQSFLEVSRYVLR 169
DB 172 NAGLLDKLOSQNEWMKNTKIILIRSLDFLOFSLRAIR 210

RESULT 9

I46590
Interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46590
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conce
A:Reference number: I46590; MUID:92360284; PMID:1497880
A:Accession: I46590
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-212 <MAT>
A:Cross-references: GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g164515
A:Genetics:
A:Gene: IL-6
C:Superfamily: interleukin-6

Query Match 11.9%; Score 106.5; DB 2; Length 212;
Best Local Similarity 22.6%; Pred. No. 0.01;
Matches 36; Conservative 33; Mismatches 85; Indels 5; Gaps 3;
QY 16 KCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIP-WAPLSSCPQALQAGC 74
DB 52 KTEELIKYLGKTSAMRKEMCEKYEKENSKEVLAENNLNPKMAEKDGCFOGFGNQETC 111
QY 75 LSQHLGSLFLYQGLQALGEGISPELGPTLDTLQLDVADPATTIWOQMEELGNAPALQPT- 133
DB 112 LMRITGLVEFQIYLDYLOKEVESNKGNGVEAQVISTKALIQTLRQKGNPKATTPNPTT 171
QY 134 -QGAMPAPAS--AFQRRAGGVLVASHLQSFLEVSRYVLR 169
DB 172 NAGLLDKLOSQNEWMKNTKIILIRSLDFLOFSLRAIR 210

RESULT 10

T09216
Interleukin-6 precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C:Accession: T09216
R:Swiderski, C.E.; Horchov, D.W.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16613
A:Accession: T09216
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-208 <SWI>
A:Cross-references: EMBL:U64794; NID:g2654387; PID:g2654388
A:Genetics:
A:Gene: IL-6
C:Superfamily: interleukin-6

C:Keywords: cytokine; growth factor

Query Match 11.2%; Score 100; DB 2; Length 208;
Best Local Similarity 21.6%; Pred. No. 0.041;
Matches 38; Conservative 35; Mismatches 95; Indels 8; Gaps 3;
QY 2 PLGPASSLPQSFLL---KCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIP 57
DB 31 PLGDETTISNGPLLTADTKYKHILKISALKNEMCNMFCKENSKEVLAENNLNLP 90
QY 58 -WAPLSSCPQALQAGCQLSHGSLFLYQGLQALGEGISPELGPTLDTLQLDVADPATT 116
DB 91 KMAEKDGCFOGFGNQETCLMKITITGLSEFQIYLEVILQNEFKGEKENIKMTQISTKVLVQI 150
QY 117 IWQOMEELGNA---PALQPTQOGAMPAPASAFQRRAGGVLVASHLQSFLEVSRYVLR 169
DB 151 LMQCKKNPEVTTPDPTAKSSLLAKLHSONEWLKNNTTHLIRSLDFLOFSLRAIR 206

RESULT 11

C82270
hypothetical protein VC0886 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82270
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, K.
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82270
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <HEI>
A:Cross-references: GB:AE004172; GB:AE003852; NID:g9655323; PIDN:AAF94048.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
A:Genetics:
A:Gene: VC0886
A:Map position: 1

Query Match 10.5%; Score 94; DB 2; Length 345;
Best Local Similarity 32.2%; Pred. No. 0.28;
Matches 38; Conservative 15; Mismatches 43; Indels 22; Gaps 6;
QY 7 SSLLPQSFLLKCLBQVRKIQDGAALQEKLC---ATYKLCHEPELVLLGHSIGIPWAPLS 62
DB 228 ASDPDLFLLAAL--VRALAGAPANILDATCDALASPACHPEVLIALA---GRSNWSLE 282
QY 63 S---CPSQALQAGCQLSQ-LHSGFLYQGLQALGEGI-----SPELGPTLDTLQ 107
DB 283 NSGRRQFLIRLAQTQNPFLNOLFADVVMPLPALRGVMLPFLHASPPELAQALEQLQ 340

RESULT 12

S03170
homeotic protein cut - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S03170
R:Blöchliger, K.; Bodmer, R.; Jack, J.; Jan, L.Y.; Jan, Y.N.
Nature 333, 629-635, 1988
A:Title: Primary structure and expression of a product from cut, a locus involved in spe
A:Reference number: S03170; MUID:88222956; PMID:2897632
A:Accession: S03170
A:Molecule type: mRNA
A:Residues: 1-2175 <BLO>
A:Cross-references: EMBL:X07985; NID:g7767; PIDN:CAA30794.1; PID:g7768
C:Genetics:
A:Gene: cut
A:Cross-references: FlyBase:FBgn0004198
C:Superfamily: homeotic protein cut; cut repeat homology; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:886-958/Domain: cut repeat homology <CU1>
F:1139-1411/Domain: cut repeat homology <CU2>
F:1617-1689/Domain: cut repeat homology <CU3>
F:1746-1802/Domain: homeobox homology <HOX>

Query Match 10.0%; Score 89.5; DB 1; Length 2175;
Best Local Similarity 23.8%; Pred. No. 6.9;
Matches 35; Conservative 20; Mismatches 61; Indels 31; Gaps 3;

QY 27 DGAALQKLCATYKLCHEPELVILGSLGIPWAPLSSCPQALQALGCLSQLHSGFLYQ 86
DB 1404 DENAVHKLVASQYKIA-PEKLMRTGSGSGSPMP-----Q 1437

QY 87 GLLQALGEGISPELPTDITLDVADPATTWQMEELGMAPALQPTQGAMPAPASAFQ 146
DB 1438 GLASKQQAASLPQKQWSELKQEPQAQHLQMQQAAMSAANQQQQ-----VAQAQQQ 1492

QY 147 RAGGVVASHLQSFLEVSRYRLHQAQ 173
DB 1493 AQAQAQAQHLQQAQQAQHLQQAQQAQ 1519

RESULT 13

A87577 oligopeptide transporter, OPT family CC2646 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: A87577

R:Nieman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A>Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: A87577

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-866 <STO>

A:Cross-references: GB:AB005673; NID:gl3424225; PIDN:AAK24613.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2646

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0361

Query Match 9.9%; Score 88.5; DB 2; Length 666;

Best Local Similarity 32.5%; Pred. No. 2.1;

Matches 37; Conservative 14; Mismatches 48; Indels 15; Gaps 4;

QY 50 LGHSLGIPWAPLSSCPQALQALGCLSQLHSGFLYQGLGIPGELGPTDITLDLQ 109

DB 196 LGASGATGIGASS--SLALMGAGHLMGITVGVANFTGLFTAWAILVPLTLVTPMEAD 253

QY 110 VADPATTWQ-QMEELG-----MAPALQPT-QGAMPAPASAFQ 150

DB 254 AATHALTWKQSVRFAGVIGAAAIWTLAKLVGPTTSGLSKSAFAAAQARKAGG 307

RESULT 14

F83292 probable sensor/response regulator hybrid PA2824 [imported] - Pseudomonas aeruginosa (st

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83292

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bu

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83292

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-786 <STO>

A:Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06212.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2824

Query Match 9.9%; Score 88.5; DB 2; Length 786;

Best Local Similarity 29.2%; Pred. No. 2.5;

Matches 50; Conservative 19; Mismatches 49; Indels 53; Gaps 10;

QY 26 DGAALQKLC-ATYKLCHEPELVILG--HSLGIPWAPLSSCPQALQALG-CLSQLHSG 81

DB 490 GGLALTRKLCAMQOGLTVESTVGLGSLFVGLPLAVSP-PLQALPLGRVIAQCSAN 548

QY 82 LFLYQGLQALGEGISPE-----LGPTDITLDVADPATTWQMEELGMA 127

DB 549 ----SGLAQLLQTLPRWGLYKRLTDDSLGHSLLDVLISDCPCL-----MGLR 595

QY 128 PALQPTQGAMPAPASAFQRRAGGVVASHLQSF--EVSRYV--LRHLAQP 174

DB 596 PSI-----GTPILLVTVAYGSLFEPALARLSPRLQRLARP 629

RESULT 15

A56610

interleukin-6 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A56610; S22162

R:Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.

DNA Seq. 2, 411-413, 1992

A>Title: Nucleotide sequence of bovine interleukin-6 cDNA.

A:Reference number: A56610; MUID:93076003; PMID:1446077

A:Accession: A56610

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <DRO>

A:Cross-references: EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194

A:Experimental source: BLV induced B cell-lymphosarcoma

A:Note: sequence extracted from NCBI backbone (NCBIP:118917)

C:Superfamily: interleukin-6

C:Keywords: cytokine

Query Match 9.6%; Score 86; DB 1; Length 208;

Best Local Similarity 20.5%; Pred. No. 0.89;

Matches 36; Conservative 37; Mismatches 95; Indels 8; Gaps 3;

QY 2 PLG---PASSLPQSFLKCLEQ-----VRKIQDGAALQKLCATYKLCHEPELVILGHSL 54

DB 31 PLGEDFNDDTTEGRLLLTTPKEALIKRMVDKISAMRKEICEKNDECESSKETLAENKL 90

QY 55 GIP-WAPLSSCPQALQALGCLSQLHSGFLYQGLQALGEGISPELGPTDITLDVADP 113

DB 91 NLPKMEKDGCCQSGFNQAICLIRTAGLLEQVILDYLQNEVEGNOENVRDLKRNRTL 150

QY 114 ATTWQMEELGMAPALQPTQGAMPAPASAFQRRAGGVVASHLQSFLEVSRYVLR 169

DB 151 IQILKQKIADLTTPATNTDLEKMQSSNEWKNKIIILRNLENFLOFSRAIR 206

Search completed: October 6, 2004, 16:07:18

Job time : 43 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 15:51:18 ; Search time 23 seconds
(without alignments)

393.922 Million cell updates/sec

Title: US-10-009-792C-19

Perfect score: 896

Sequence: 1 TPLGPASSLPQSFLKCLEQ.....SHLQSFLEVSRYRLHLAQP 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	884.5	98.7	207	1 CSF3_HUMAN	P09919 homo sapien
2	744	83.0	194	1 CSF3_FELCA	O02708 felis silve
3	738	82.4	174	1 CSF3_SHEEP	Q28746 ovis aries
4	734	81.9	175	1 CSF3_CANFA	P35834 canis fami
5	727	81.1	195	1 CSF3_BOVIN	P35833 bos taurus
6	702	78.3	195	1 CSF3_PIG	O02837 sus scrofa
7	641	71.5	208	1 CSF3_MOUSE	P09920 mus musculu
8	304	33.9	201	1 MGF_CHICK	P13854 gallus gall
9	106.5	11.9	212	1 IL6_PIG	P26893 sus scrofa
10	101	11.3	205	1 IL6_ORCOR	Q28747 orcinus orc
11	100	11.2	208	1 IL6_HORSE	Q95181 equus cabal
12	95	10.6	208	1 IL6_FELCA	P41683 felis silve
13	89.5	10.0	2175	1 HMCU_DROME	P10180 drosophila
14	86	9.6	208	1 IL6_BOVIN	P26892 bos taurus
15	84.5	9.4	209	1 IL6_PROVI	Q28819 phoca vitul
16	84	9.4	208	1 IL6_CAPHI	Q28319 capra hircu
17	84	9.4	208	1 IL6_SHEEP	P29455 ovis aries
18	80.5	9.0	406	1 SYT2_ABRPE	Q9YF33 aeropyrum p
19	79.5	8.9	207	1 IL6_CANFA	P41323 canis fami
20	78.5	8.8	300	1 GGPFP_MOUSE	Q9Wtn0 m geranylge
21	78	8.7	316	1 KXSE_PSEAE	P29364 pseudomonas
22	77	8.6	247	1 RECO_NEIGO	Q9Zhy2 neisseria g
23	76.5	8.5	195	1 CNTF_CHICK	Q20211 gallus gall
24	76.5	8.5	294	1 GPPP_BOVIN	P56966 b geranylge
25	76.5	8.5	383	1 ARGE_SHIFL	P59600 shigella fl
26	76.5	8.5	506	1 ER11_BRANA	O65727 brassica na
27	76	8.5	1704	1 ABC3_HUMAN	Q99758 homo sapien
28	75.5	8.4	156	1 KAMC_SACHI	P25919 saccharopol
29	75.5	8.4	3027	1 POLG_EYFVL	Q05057 parsnip yel
30	75	8.4	199	1 IL11_HUMAN	Q20809 homo sapien
31	75	8.4	330	1 OXF2_HUMAN	P08nh61 homo sapien
32	74.5	8.3	212	1 IL6_HUMAN	P52231 homo sapien
33	74	8.3	367	1 CD5S_HUMAN	Q13319 homo sapien

34	74	8.3	2504	1 PAS_HUMAN	P49327 homo sapien
35	73.5	8.2	383	1 ARGE_ECOLI	P23908 escherichia
36	73.5	8.2	737	1 RECG_MYCTU	P95122 mycobacteri
37	73	8.1	204	1 CTF2_MOUSE	P83714 mus musculu
38	73	8.1	836	1 VG26_BPM15	Q05233 mycobacteri
39	72.5	8.1	203	1 Y626_VIBVU	P59257 vibrio vuln
40	72.5	8.1	383	1 ARGE_ECO57	Q8X742 escherichia
41	72.5	8.1	383	1 ARGE_ECOL6	Q8fb97 escherichia
42	72	8.0	1399	1 Z291_HUMAN	Q9BY12 homo sapien
43	71.5	8.0	300	1 GGPP_HUMAN	O95749 h geranylge
44	71.5	8.0	518	1 ER12_BRANA	O65726 brassica na
45	71.5	8.0	836	1 GCSR_HUMAN	Q99062 homo sapien

ALIGNMENTS

RESULT 1					
CSF3_HUMAN					
ID	CSF3_HUMAN	STANDARD;	PRT;	207 AA.	
AC	P09919;				
DT	01-MAR-1989	(Rel. 10, Created)			
DT	01-MAR-1989	(Rel. 10, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripotin)				
DE	(Filgrastim) (Lenograstim).				
GN	CSF3				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86118679; PubMed=3484805;				
RA	Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,				
RA	Hirata Y., Kubota N., Oheda M., Nomura H., Yamazaki T.;				
RT	"Molecular cloning and expression of cDNA for human granulocyte				
RT	colony-stimulating factor.";				
RL	Nature 319:415-418(1986).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86220137; PubMed=2423327;				
RA	Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,				
RA	Oheda M., Nomura H., Yamazaki T.;				
RT	"The chromosomal gene structure and two mRNAs for human granulocyte				
RT	colony-stimulating factor.";				
EMBO	J. 5:575-581(1986).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87196936; PubMed=3494801;				
RA	Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,				
RA	Warren M.K.;				
RT	"Expression of granulocyte colony-stimulating factor by human cell				
RT	lines.";				
RL	J. Leukoc. Biol. 41:302-306(1987).				
RN	[4]				
RP	SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.				
RA	Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,				
RA	Nickerson D.A.;				
Submitted	(JUN-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE OF 19-207 FROM N.A.				
RX	MEDLINE=86151684; PubMed=2420009;				
RA	Souza L.N., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,				
RA	Murdoch D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,				
RA	Barendt J., Platzer E., Moore M.A.S., Mettelmann R., Welte K.;				
RT	"Recombinant human granulocyte colony-stimulating factor: effects on				
RT	normal and leukemic myeloid cells.";				
Science	232:61-66(1986).				
RN	[6]				
RP	CARBOHYDRATE-LINKAGE SITE.				
RA	MEDLINE=93293942; PubMed=7685769;				
RA	Clogston C.L., Hu S., Boone T.C., Lu H.S.;				

RT "Glycosidase digestion, electrophoresis and chromatographic analysis
of recombinant human granulocyte colony-stimulating factor glycoforms
produced in Chinese hamster ovary cells.";
J. Chromatogr. A 637:55-62(1993).
[7]
RP STRUCTURE BY NMR.
RX MEDLINE=93106200; PubMed=1281794;
RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
RT "Secondary structure of human granulocyte colony-stimulating factor
derived from NMR spectroscopy.";
RL FEBS Lett. 314:435-439(1992).
[8]
RP STRUCTURE BY NMR.
RX MEDLINE=94304859; PubMed=7518249;
RA Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.;
RT "Structure and dynamics of the human granulocyte colony-stimulating
factor determined by NMR spectroscopy. Loop mobility in a four-helix-
bundle protein.";
RL Biochemistry 33:8453-8463(1994).
[9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93281718; PubMed=7685117;
RA Hill C.P., Osslund T.D., Eisenberg D.;
RT "The structure of granulocyte-colony-stimulating factor and its
relationship to other growth factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CSF INDUCES GRANULOCYTES.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P09919-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P09919-2; Sequence=VSP_002673;
CC -!- PTM: O-GLYCAN CONSISTS OF GAL-GALNAc DISACCHARIDE WHICH CAN BE
MODIFIED WITH UP TO TWO SIALIC ACID RESIDUES (DONE IN
RECOMBINANTLY EXPRESSED G-CSF FROM CHO CELLS).
CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
(Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
neutropenia (a disorder characterized by an extremely low number
of neutrophils in blood).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- CAUTION: REP. 4 MISQUOTES THE GENE NAME AS "CSF1".
CC -!- DATABASE: NAME=Neupogen/Granulokine;
CC NOTE=Clinical information on Neupogen/Granulokine;
CC WWW="http://www.neupogen.com/".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; X03438; CAA27168.1; -
CC EMBL; M13008; AAA03056.1; -
CC EMBL; X03655; CAA27291.1; -
CC EMBL; X03655; CAA27290.1; -
CC EMBL; AF388025; AAK62469.1; -
CC EMBL; M17706; AAA35882.1; -
CC PIR; A24573; A24573.
CC PIR; A25093; FQHUGL.
CC PDB; 1RHG; 31-JAN-94.
CC PDB; 1GNC; 31-JUL-94.
CC PDB; 1CD3; 08-MAR-00.
CC PDB; 1PGR; 08-MAR-00.
CC Genew; HGNC:2438; CSF3.

DR MM; 138970; -. C:extracellular space; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep...; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal; Alternative splicing;
KW Polymorphism; Pharmaceutical; 3D-structure.
FT SIGNAL 1 30 GRANULOCYTE COLONY-STIMULATING FACTOR.
FT CHAIN 31 207
FT DISULFID 69 75
FT DISULFID 97 107
FT CARBOHYD 166 166
FT VARSPLIC 66 68
FT VARIANT 157 157
FT VARIANT 174 174
FT VARIANT 41 65
FT HELIX 69 71
FT HELIX 77 86
FT TURN 87 88
FT HELIX 105 124
FT TURN 125 127
FT TURN 130 132
FT HELIX 133 156
FT TURN 157 158
FT HELIX 176 203
FT TURN 204 204
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;
Query Match 98.7%; Score 884.5; DB 1; Length 207;
Best Local Similarity 98.3%; Pred. No. 3.1e-74;
Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
Qy 1 TPLGPASSLPQSFLKCLEQVRXIQDGAALQKEL---CATYKLCHEPELVLLGHSLGIP 57
Db 31 TPLGPASSLPQSFLKCLEQVRXIQDGAALQKELVSECATYKLCHEPELVLLGHSLGIP 90
Qy 58 WAPLSSCPQALQIAGCLSQLHSLGLYQGLQALGSLSPGLPTDQLQDVADPATTI 117
Db 91 WAPLSSCPQALQIAGCLSQLHSLGLYQGLQALGSLSPGLPTDQLQDVADPATTI 150
Qy 118 WQWMEELGMAPALQPTQGMPPAFASAFQRRAGGVLVASHLQSFLEYSYRVLRLAQP 174
Db 151 WQWMEELGMAPALQPTQGMPPAFASAFQRRAGGVLVASHLQSFLEYSYRVLRLAQP 207
RESULT 2
CSF3_FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
GN Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=European shorthair; TISSUE=Lung;
RX MEDLINE=21389237; PubMed=11497496;
RA Dunham S.P., Onions D.B.;

```

RT "Isolation, nucleotide sequence and expression of a cDNA encoding
RT feline granulocyte colony-stimulating factor.";
RL Cytokine 14:347-351(2001).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CC CSF INDUCES GRANULOCYTES (BY SIMILARITY).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y08558; CNA69853.1; -
CC FIRM; T09255; T09255.
CC HSP; P35834; LBGE.
CC InterPro; IPR003629; GCSF_MGF.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC ProDom; PD008388; GCSF_MGF; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
FT NON TER 1
FT SIGNAL <1 20 POTENTIAL.
FT CHAIN 21 194 GRANULOCYTE COLONY-STIMULATING FACTOR.
FT DISULFID 56 62 BY SIMILARITY.
FT DISULFID 84 94 BY SIMILARITY.
FT CARBOHYD 153 153 O-LINKED (GALNAAC... ) (BY SIMILARITY).
SQ SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;

Query Match 83.0%; Score 744; DB 1; Length 194;
Best Local Similarity 81.0%; Pred. No. 2.3e-61;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 21 TPLGPTSSLPQSFLKLCLEQVRKVQADGTALQERLCRAHKLCHPEELVLLGHALGIPQAP 80
QY 61 LSSCPSQALQACLSQLHSGFLYQGLLQALAGISPELGTDLTLDLVADPATTIWQQ 120
DB 81 LSSCPSQALQACLSQLHSGFLYQGLLQALAGISPELGTDLTLDLVADPATTIWQQ 140
QY 121 MEELGNAPALQPTQGAAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
DB 141 MEDVGMAFVPTQGTMTFTTSAFQRRAGGVLVASHLQSFLEVSVYRVLRLHFTKP 194

RESULT 3
CSF3 SHEEP
ID CSF3 SHEEP STANDARD; PRT; 174 AA.
AC Q28746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN CSF3.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=95102116; PubMed=7528579;
RA O'Brien P.M., Seow H.F., Rothe J.S., Wood P.R.;
RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT factor cDNA.";
RL DNA Seq. 4:339-342(1994).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CC CSF INDUCES GRANULOCYTES (BY SIMILARITY).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L07939; AAA68006.1; -
CC PIR; T10268; T10268.
CC HSP; P35833; LBGC.
CC InterPro; IPR003629; GCSF_MGF.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC ProDom; PD008388; GCSF_MGF; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Cytokine; Growth factor; Glycoprotein.
FT DISULFID 36 42 BY SIMILARITY.
FT DISULFID 64 74 BY SIMILARITY.
FT CARBOHYD 133 133 O-LINKED (GALNAAC... ) (BY SIMILARITY).
SQ SEQUENCE 174 AA; 18806 MW; BASAA8F8D23ACD1E CRC64;

Query Match 82.4%; Score 738; DB 1; Length 174;
Best Local Similarity 82.2%; Pred. No. 7.3e-61;
Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
DB 1 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAP 60
QY 61 LSSCPSQALQACLSQLHSGFLYQGLLQALAGISPELGTDLTLDLVADPATTIWQQ 120
DB 61 LSSCPSQALQACLSQLHSGFLYQGLLQALAGISPELGTDLTLDLVADPATTIWQQ 120
QY 121 MEELGNAPALQPTQGAAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 174
DB 121 MEDVGMAFVPTQGTMTFTTSAFQRRAGGVLVASHLQSFLEVSVYRVLRLHAE 174

RESULT 4
CSF3 CANFA
ID CSF3 CANFA STANDARD; PRT; 175 AA.
AC P35834;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN CSF3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg D.;

```


DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 201 MYELOMONOCYTIC GROWTH FACTOR.
FT DISULFID 61 67 BY SIMILARITY.
FT DISULFID 89 99 BY SIMILARITY.
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 201 AA; 22373 MW; 240A8DD21B424AE6 CRC64;

Query Match 33.9%; Score 304; DB 1; Length 201;
Best Local Similarity 40.6%; Pred. No. 6e-21;
Matches 67; Conservative 28; Mismatches 68; Indels 2; Gaps 1;

QY 11 QSFLLKLEQVRKIQDGAALQEKLCATYKLPHELVLLGHSIGIPWAPLSQSQALQ 70
Db 36 QLFELKNELEFTRKIRGDVAALQRAVCDTFLQCTEELQVDPHLVQAPLQDQCHKRGFQ 95
QY 71 LAGCLSQLHSLFLYQGLLQALLEGISPELGLPTLDTLQLDVADFATTIWOQMEELGNAPAL 130
Db 96 AEVCTQIRAGDHAYHDSLGAVLRDPNHTTVETLQDAANLSSNIQQOMEDLGLDTVT 155
QY 131 QPTQ--GAMPAFASAFQRRAGGVVASHLQSFLEVSRYVRHLAQ 173
Db 156 LPAEQSRPPPTFGSPFQQQVGGFFILANFQFLETAYRALRHLAR 200

RESULT 9
IL6_PIG
ID IL6_PIG STANDARD; PRT; 212 AA.
AC P26893; Q95KN6;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91338547; PubMed=1873476;
RA Richards C., Saklatvala J.;
RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
RL expression of mRNA in synovial fibroblasts in vitro.";
RN Cytokine 3:269-276 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92360284; PubMed=1497880;
RA Mathialagan N., Bixby J.A., Roberts M.R.;
RT "Expression of interleukin-6 in porcine, ovine, and bovine
RL preimplantation conceptuses";
RN Mol. Reprod. Dev. 32:324-330 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace x Meishan; TISSUE=Blood;
RA Liu S., Meng M., Gao R.;
RT "Cloning and expression of interleukin 6 gene from Landrace x Meishan
RL hybrid swine";
CC Submitted (SFP-2000) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC SUBCELLULAR LOCATION: Secreted.
CC SIMILARITY: Belongs to the IL-6 superfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

FT DISULFID 100 110 BY SIMILARITY.
FT CARBOHYD 169 169 O-LINKED (GALNAC. . .) (BY SIMILARITY).
SQ SEQUENCE 208 AA; 22421 MW; 0B36222135C906DB CRC64;

Query Match 71.5%; Score 641; DB 1; Length 208;
Best Local Similarity 75.9%; Pred. No. 7.3e-52;
Matches 129; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

QY 3 LCPASLPQSLKLEQVRKIQDGAALQEKLCATYKLPHELVLLGHSIGIPWAPLS 62
Db 39 LPPSLPLPSFLKLEQVRKIQDGSVLLQGLCATYKLPHELVLLGHSIGIPKASLS 98
QY 63 SCPSQALQAGLSQLHSLFLYQGLLQALLEGISPELGLPTLDTLQLDVADFATTIWOQME 122
Db 99 GCSQALQOQTCLSQLHSLGCLYQGLLQALSGISPALPTLDTLQLDVANFATTIWOQME 158
QY 123 ELGMAPALQPTQGMAPAFASAFQRRAGGVVASHLQSFLEVSRYVRHLA 172
Db 159 NLGVAPTQVQTSAMPFTSAFQRRAGGVVASHLQSFLEVSRYVRHLA 208

RESULT 8
MGF_CHICK
ID MGF_CHICK STANDARD; PRT; 201 AA.
AC P13854;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myelomonocytic growth factor precursor (MGF).
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89231616; PubMed=2785450;
RA Leutz A., Damm K., Sterneck E., Kowenz E., Ness S., Frank R.,
RA Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.; factor (CMGF)
RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
RL reveals relationship to interleukin 6 and granulocyte colony
RN stimulating factor";
RN EMBO J. 8:175-181 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92195319; PubMed=1549124;
RA Sterneck E., Blattner C., Graf T., Leutz A.;
RT "Structure of the chicken myelomonocytic growth factor gene and
RL specific activation of its promoter in avian myelomonocytic cells by
RN protein kinases";
RN Mol. Cell. Biol. 12:1728-1735 (1992).
RN [3]
RP FUNCTION: HEMATOPOIETIC GROWTH FACTOR THAT STIMULATES THE
CC PROLIFERATION AND COLONY FORMATION OF NORMAL AND TRANSFORMED AVIAN
CC CELLS OF THE MYELOID LINEAGE.
CC SUBCELLULAR LOCATION: Secreted.
CC SIMILARITY: Belongs to the IL-6 superfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL; M85034; AAA48694.1; -;
CC EMBL; X14477; CAA32639.1; -;
CC PIR; A42247; A42247.
CC HSP; P35834; IBGD.
CC InterPro; IPR003629; GCSF MGF.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC Pfam; PF00489; IL6; 1
CC PRINTS; PR00433; IL6GCSFMGF.

[illegible]

Tue Oct 12 09:18:49 2004

Search completed: October 6, 2004, 16:04:29
Job time : 25 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 15:58:27 ; Search time 117 Seconds
(without alignments)
469.232 Million cell updates/sec

Title: US-10-009-792C-19

Perfect score: 896

Sequence: 1 TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEVSRYVRHLAQP 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL_25.*

2: sp_archaea.*

3: sp_bacteria.*

4: sp_fungi.*

5: sp_human.*

6: sp_invertebrate.*

7: sp_mammal.*

8: sp_mic.*

9: sp_organelle.*

10: sp_phage.*

11: sp_plant.*

12: sp_rodent.*

13: sp_virus.*

14: sp_vertebrate.*

15: sp_unclassified.*

16: sp_rvirus.*

17: sp_bacteriap.*

18: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	896	100.0	200	Q8N4W3	Q8N4W3 homo sapien
2	744	83.0	195	Q9GJU0	Q9GJU0 felis silve
3	634	70.8	214	P97712	P97712 rattus norv
4	511	57.0	127	Q8MKE0	Q8MKE0 equus cabal
5	111	12.4	241	Q90Y10	Q90Y10 gallus gall
6	110.5	12.3	212	Q8MJ75	Q8MJ75 sus scrofa
7	108	12.1	208	Q8XT80	Q8XT80 delphinapte
8	96	10.7	189	Q4H2A5	Q4H2A5 homo sapien
9	94.5	10.5	455	16 Q8D706	Q8D706 vibrio vuln
10	94	10.5	345	16 Q9KTL6	Q9KTL6 vibrio chol
11	93	10.4	189	4 Q9NPF7	Q9NPF7 homo sapien
12	89.5	10.0	214	6 Q8MKE5	Q8MKE5 sus scrofa
13	88.5	9.9	666	16 Q9A523	Q9A523 caulobacter
14	88.5	9.9	786	16 Q9I019	Q9I019 pseudomonas
15	88.5	9.9	1931	2 Q8RJY3	Q8RJY3 stigmatella
16	86	9.6	502	8 Q34008	Q34008 beta vulgar

17	86	9.6	788	11	Q8CF87	Q8cf87 mus musculu
18	86	9.6	850	11	Q7TQ21	Q7tq21 mus musculu
19	86	9.6	851	11	Q8CF88	Q8cf88 mus musculu
20	86	9.6	852	11	Q811T9	Q811t9 mus musculu
21	85.5	9.5	211	6	Q865W7	Q865w7 canelus bac
22	85.5	9.5	1288	10	Q8LQR8	Q8lqr8 oryza sativ
23	85	9.5	193	6	Q9N2H9	Q9n2h9 sus scrofa
24	84.5	9.4	211	6	Q865X6	Q865x6 lama glama
25	84	9.4	175	6	Q9TTH4	Q9tth4 actus nigri
26	84	9.4	209	6	Q9TTH3	Q9tth3 actus lemur
27	84	9.4	274	17	Q29363	Q29363 archaeoglob
28	84	9.4	290	4	Q9P0S7	Q9p0s7 homo sapien
29	84	9.4	641	17	Q8ZTH1	Q8zth1 pyrobaculum
30	83.5	9.3	212	6	Q8MKH0	Q8mkh0 salmari sci
31	83.5	9.3	846	11	Q923R8	Q923r8 cavia porce
32	83.5	9.3	846	11	Q8CHL9	Q8chl9 cavia porce
33	82.5	9.2	207	6	Q9MYZ7	Q9myz7 canis fami
34	82.5	9.2	207	6	Q28403	Q28403 enhydra lut
35	82.5	9.2	327	13	Q7ZTY0	Q7zty0 brachydanio
36	81	9.0	244	2	Q8GMH8	Q8gmh8 streptomyc
37	81	9.0	5457	2	Q83VS1	Q83vs1 pseudomonas
38	80.5	9.0	641	4	Q94927	Q94927 homo sapien
39	80.5	9.0	3729	2	O33956	O33956 streptomyc
40	80	8.9	355	10	Q9AV51	Q9av51 oryza sativ
41	80	8.9	355	10	Q7XDB0	Q7xdb0 oryza sativ
42	80	8.9	474	16	Q9RX39	Q9rx39 deinococcus
43	80	8.9	477	4	Q9NT11	Q9nt11 homo sapien
44	80	8.9	811	16	Q8DGS2	Q8dgs2 synechococc
45	80	8.9	966	4	Q8NDG1	Q8ndg1 homo sapien

ALIGNMENTS

RESULT 1

Q8N4W3 PRELIMINARY; PRT; 200 AA.
ID Q8N4W3
AC Q8N4W3
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC033245; AAH33245.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6_1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Hypothetical protein.
SQ SEQUENCE 200 AA; 21543 MW; 8648AA55B329A96C CRC64;

Query Match 100.0%; Score 896; DB 4; Length 200;

Best Local Similarity 100.0%; Pred. No. 1.9e-77;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPLGPASSLPQSFLLKCLEQVRIQDGAALQEKLCATYKLCHEPVLVILGSLGIPWAP 60

Db 27 TPLGPASSLPQSFLLKCLEQVRIQDGAALQEKLCATYKLCHEPVLVILGSLGIPWAP 86

```

P97712          PRELIMINARY;          PRT;   214 AA.
ID   AC
AD   P97712;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Granulocyte colony stimulating factor.
DE   Rattus norvegicus (Rat).
OS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RX   [1]
RN   SEQUENCE FROM N.A.
RP   MEDLINE=97074656; PubMed=9917083;
RA   Han S.W., Ramesh N., Osborne W.R.;
RT   "Cloning and expression of the cDNA encoding rat granulocyte colony-
RT   stimulating factor.";
RL   Gene 175:101-104(1996).
EMBL   U37101; AAC52915.1; -.
DR   PIR; JC5043; JC5043.
DR   HSP; P09919; 1RHG.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003629; GCSF_MGF.
DR   InterPro; IPR003573; IL6_MGF_GCSF.
DR   Pfam; PF00489; IL6; 1.
DR   PRINTS; PR00433; IL6GCSFMGF.
DR   ProDom; PD008388; GCSF_MGF; 1.
DR   SMART; SM00126; IL6; 1.
DR   PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ   SEQUENCE 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Watch              70.8%; Score 634; DB 11; Length 214;
Best Local Similarity    73.8%; Pred. No. 1.9e-52;
Matches 127; Conservative 10; Mismatches 35; Indels 0; Gaps 0

QY   3  LCPASSLPQSFLKLCLEQVKRIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWAPLS 62
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   30  LPPSLPLPRSFLLKSLQVKRIQARNTLELQLCATYKLCHPPELVLFHGLGIPKASLS 89

QY   63  SCPSQALQALQCLSQLHSGFLFYQGLLOALEGISPELGPFTLDLQLDVAADPATTIWOQME 122
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   90  SCSQALQOQLKSLHSGFLFYQGLLOALAGSSSLAPTLDMLHLDVDNFATTIWOQME 149

QY   123  ELGWAPALQPTQGGAMPAFASAFORAGGVIVASHLQSFLEVSRYVLRHLAQP 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   150  SLGVAPTQPTQSTMPFTSAFQRRAGGVIVTSYLSQSFLETAHALLHLPRP 201

RESULT 4
Q8MKE0          PRELIMINARY;          PRT;   127 AA.
ID   Q8MKE0
AC   Q8MKE0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Granulocyte colony-stimulating factor.
DE   G-CSF.
GN   Equus caballus (Horse).
OS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RX   [1]
RN   SEQUENCE FROM N.A.
RA   Noronha L.E., Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AF503365; AAM34205.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.

```

```
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 127 AA; 13657 MW; 25559C2569802077 CRC64;

Query Match
Best Local Similarity 57.0%; Score 511; DB 6; Length 127;
Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 48 VLLHSLGIPWAPLSSCPQALQLAGCLSQLHSLGLFLYQGLLQALEGISPELPGTLDPLQ 107
DB 1 MLLHSLGIPQPLSSCPQALQLAGCLSQLHSLGLFLYQGLLQALEGISPELPGTLDPLQ 60
QY 108 LDVADPATTIWOOMELGMALPGTQGMAMPAPAFASAFORRAGGVLVASHLOFLEVSRYV 167
DB 61 LDVTPATTIWOOMEDLGAVPVQPTGMPMTAFASAFORRAGGVLVASHLORFLELAYRG 120
QY 168 LRHLAQP 174
DB 121 LRYLAEP 127

RESULT 5
ID Q90Y10 PRELIMINARY; PRT; 241 AA.
AC Q90Y10;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-6 precursor.
GN IL-6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RA Schneider K., Klaas R., Kaspers B., Stacheli P.;
RT "Chicken interleukin-6: cDNA structure and biological properties.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
RA Wigley P.;
RT "Differential cytokine expression in avian cells in response to
RT invasion by Salmonella typhimurium, Salmonella enteritidis and
RT Salmonella gallinarum.";
RL Microbiology 146:3217-3226(2000).
RN [3]
SEQUENCE FROM N.A.
RA Kaiser P.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309540; CAC40812.1; -.
DR EMBL; AJ250838; CAC15566.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Signal.
FT SIGNAL 1 47 POTENTIAL.
FT CHAIN 48 241 MATURE CHIL-6.

SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;

Query Match
Best Local Similarity 12.4%; Score 111; DB 13; Length 241;
Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;

QY 3 LGPASSLP-----QSFLKCLEQVRKIQDGAALQEKLCATYKLCH 43
DB 41 LPPAAAVPLPAAADSSGEVGLSEEGARRALLDCEPLARVLDRVAVQLQDEMCKFTVCE 100
QY 44 PEELVLGHSLGIPWAPLSSCPQALQLAG-----CLSQLHSLGLFLYQGLLQALEGISPE 98
DB 101 NSMEMVRNNINLP-----KVTEEDGCLLAGFDEBKCTLLSSGLFAFYLYEFTQTFDS 156
QY 99 LGPTLDTLDVADPATTIWOOMELGMALPGTQGMAMPAPAFASAFORRAGGV 152
DB 157 EKQNVESLCYSTRKLAATIRQMV-----INPDEVWIP--DAAQKSLANLKSDDKW 206
QY 153 ---VASHL-----QSFLVSRYVLRHL 171
DB 207 IEXTVHLILRDTSMKTVRAVRYL 233

RESULT 6
ID Q8XJ75 PRELIMINARY; PRT; 212 AA.
AC Q8XJ75;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RT "Sequencing of porcine IL-6 in Korea.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF518322; AAM74938.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E7030BCFD77 CRC64;

Query Match
Best Local Similarity 12.3%; Score 110.5; DB 6; Length 212;
Matches 37; Conservative 32; Mismatches 85; Indels 5; Gaps 3;

QY 16 KCLEQVRKIQDGAALQEKLCATYKLCHPEELVLGHSLGIP-WAPLSSCPQALQLAG 74
DB 52 KTEELIKYLKISAWREEMCEKCNSEKVENLNNLNPMAEKDCGCFSGFNQETC 111
QY 75 LSQHLHSLGLYQGLLQALEGISPELPGTLDVADPATTIWOOMELGMALPGT- 133
DB 112 LMEITITGLVEFYIYLDYLQKEYESNKGNEAVQISTKALITLROKGNPKDATTNPPT 171
QY 134 -QGMAMPAPAS--AFORRAGGVLVASHLOFLEVSRYVLR 169
DB 172 NAGLLDKLOSQNEWMKNTKIILRLSLDFLOQFSLEAIR 210

RESULT 7
Q9XT80
```

```

ID Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodactyla; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
SEQUENCE FROM N.A.
RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -
DR HSSP; P05231; IALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SEQUENCE 208 AA; 23456 MW; 81CC85C6E80399C4 CRC64;
SQ
Query Match 12.1%; Score 108; DB 6; Length 208;
Best Local Similarity 21.3%; Pred. No. 0.025;
Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;
QY 21 VRKIQDGAALQKLCATYKLCPELVLLGHSLGIP-WAPLSSCPQALQAGLCLSLH 79
DB 52 IKYLGKISAMRKEMCEKYDKKENSEKEALNNLPLPWAEXKDGFCQSGFNQETCLMRIT 111
QY 80 SGLFYQGLQLQALEGISPELGTDLTLDQVADPATTIQQMEELGMAPALQTOGA--- 136
DB 112 TGLEYQIVLDYQNEVEYEGDKSIEAVQISIKALQILRKQKNPDEVTPDPTNASIM 171
QY 137 --MPAFASFORAGGVIVASHLQSPLEVSRYVLR 169
DB 172 NNLQSQNDMMRNTKIILRLSLNLEPLQFSLRAVR 206
RESULT 8
ID Q9H2A5 PRELIMINARY; PRT; 189 AA.
AC Q9H2A5;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Interleukin 23 p19 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=20567322; PubMed=11114383;
RA Opmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
RA Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
RA Kastelein R.A.;
RT "Novel p19 Protein Engages IL-12p40 to Form a Cytokine, IL-23, with
RT Biological Activities Similar as Well as Distinct from IL-12."
RL Immunity 13:715-725(2000).
DR EMBL; AF301620; AAG37232.1; -.

```

```

DR Genew; HGNC:15488; IL23A.
SQ SEQUENCE 189 AA; 20744 MW; BF5C0F42D4C1E3A CRC64;
Query Match 10.7%; Score 96; DB 4; Length 189;
Best Local Similarity 26.1%; Pred. No. 0.31;
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;
QY 14 LLKCLEQVRKIQGDGA-----ALQEKLCATYKLCPELVLLGH-----SLG 55
DB 12 LLPWTAQGRAVPGSSPAWTCQQLSQKLCITLAWSAHP-----LVGHMDLRBEGDBETND 67
QY 56 IPWAPL-SSCPQALQ--LAGCLSQLHSGFLYQGL--QALEGISPELGTDLTLDQV 110
DB 68 VPHIQCGDGDPOGLRDNQSFQCLRIHQGLIFVEKLLGSDITFG-EPSLLPSPVAQLHA 126
QY 111 ADFATTIQQME-----ELGNAPALQTOGMAPAFASFORAGGVIVASHLQSPLEVSRY 166
DB 127 SLGLSQLQPEGHHWETQIIPSLSPSQ-----PWQRLILRFKILRSLOAFVAAR 178
QY 167 VLRH 170
DB 179 VFAH 182
RESULT 9
Q8D706 PRELIMINARY; PRT; 455 AA.
ID Q8D706
AC Q8D706;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Biopolymer transport protein.
GN VY20363.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
SEQUENCE FROM N.A.
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016809; AAC07321.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002898; MctA_EXDS.
DR Pfam; PF01619; MctA_Exdb; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 455 AA; 49446 MW; 241A87B1CDB8E942 CRC64;
Query Match 10.5%; Score 94.5; DB 16; Length 455;
Best Local Similarity 24.6%; Pred. No. 1.2;
Matches 43; Conservative 15; Mismatches 40; Indels 77; Gaps 7;
QY 6 ASSLPQSFLKLCLEQVRKIQ---GDGAALQEKLCATYKLCPELVLLGH----- 52
DB 140 AQLSPDIAQLKTLWHVWQQQIVASGEMRALQVRLINAEVVEPTDVNLCNFALLAPQGF 199
QY 53 -----SLGIPWAPLSSCPQALQAGCLSQLHSGFLYQGLQALEGISPELGTDLT 105
DB 200 VNMNSDKGFAPYAKL-----PGCAPTLDT 224
QY 106 LQLDVADPATTIQQMEELGMAPAL-QTOGM-----PAPASAFORAGGV 152
DB 225 L-----RSQHEISMTVPLIDPTEGVLEQVYAHSPSLDRF--AAGGV 265
RESULT 10
Q9KTL6 PRELIMINARY; PRT; 345 AA.
ID Q9KTL6

```


Q9KTL6;
 01-OCT-2000 (Tremblrel. 15, Created)
 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein VC0886.
 GN VC0886.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT cholerae".
 RL Nature 406:477-483 (2000).
 DR EMBL; AE004172; AAF94048.1; --
 DR PIR; C82270; C82270.
 DR TIGR; VC0886; --
 DR InterPro; IPR001303; Aldolase II.N.
 KW Hypothetical protein, Complete proteome.
 SQ SEQUENCE 345 AA; 38781 MW; E446D7798ADA7E01 CRC64;

Query Match 10.5%; Score 94; DB 16; Length 345;
 Best Local Similarity 32.2%; Pred. No. 0.97;
 Matches 38; Conservative 15; Mismatches 43; Indels 22; Gaps 6;

QY 7 SSLPSGLKLEQVRKIQGGALQKLC---ATYKLCHEPELVLLGHSLGIPWAPLS 62
 228 ASDPLFLAL--VRLAGAPANILDTCDAILASPAICPEVLIALA---GRSWSLE 282

QY 63 S---CPSQALQAGLSQ-LHSGFLYQGLLQALEGI-----SPELGTLDLQ 107
 283 NSGRAQREFLRLAQTONQFLNQLFADVVMPLALRGVMLPLLHASPPELAQALEQLQ 340

RESULT 11
 Q9NPF7 PRELIMINARY; PRT; 189 AA.
 ID Q9NPF7
 AC Q9NPF7
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-WAR-2003 (Tremblrel. 23, Last annotation update)
 DE SGRF precursor.
 GN SGRF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Hirata Y., Kosuge Y.;
 RT "SGRF: a novel member of the IL-6/G-CSF family";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030000; BAA93686.1; --
 DR EMBL; AB030001; BAA93687.1; --
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 20 189 SGRF.
 SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;

Query Match 10.4%; Score 93; DB 4; Length 189;
 Best Local Similarity 26.1%; Pred. No. 0.59;
 Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 14 LLKCLEQVRKIQGGALQKLCATYKLCHEPELVLLGH-----SLG 55
 12 LLPTAQGRAVFGSSPAWTCQQLSKLCTLAWSAHP-----LVGHMDLRREGDETTND 67
 QY 56 IPWAPL-SSCPQALQ--LAGCLSQLHSLGFLYQGLL--QALEGISPELGTLDLQLDV 110
 68 VPHIQCGDCDPQGLRDSQFLQRIHQGLIPEYKLLGSDIFTG-EPSSLPSVPGQLHA 126
 QY 111 ADPATTIWOQMB---ELGMAPALOPTQGMAPAFASAFORRAGGVLVASHLQSFLEVS 166
 127 SLLGLSQQLOPEGHWHWETQIIFSLSPSQ-----PWQRLRLRKFILRSQAFAVAAR 178
 QY 167 VLRH 170
 Db 179 VFAH 182

RESULT 12
 Q8MKES PRELIMINARY; PRT; 214 AA.
 ID Q8MKES
 AC Q8MKES
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Interleukin-6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Wu M., Gao R., Li J., Meng M., Long Z., Tang M., Liu S.;
 RT "Cloning and sequence analysis of interleukin-6 gene from Chenghua
 RT swine".
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF493592; AAM27192.1; --
 DR GO; GO:0005576; Extracellular; IEA.
 DR GO; GO:0005125; Fc cytokine activity; IEA.
 DR GO; GO:0005138; Fc interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P. Immune response; IEA.
 DR InterPro; IPR003573; IL6 MGF GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SMC0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 214 AA; 23765 MW; 50849FB04D0BDD7F CRC64;

Query Match 10.0%; Score 89.5; DB 6; Length 214;
 Best Local Similarity 23.0%; Pred. No. 1.5;
 Matches 28; Conservative 25; Mismatches 68; Indels 1; Gaps 1;

QY 16 KCLEQVRKIQGGALQKLCATYKLCHEPELVLLGHSLGIP-WAPLSSCPQALQAGC 74
 52 KTEELIKYILGKISANRKMCKEYKCNSEKVEAENLNLPKVAEKDGFQSGFNQETC 111

QY 75 LSQHLGFLYQGLLQALEGISPELGTLDLQDVADPATTIWOQMBELGVAPALQPTQ 134
 112 LMRITTLGVFQIYLDYLOKYESNKGNEAVQISTKALIQTLRQKGNPKATTENPTT 171

QY 135 GA 136
 Db 172 NA 173

RESULT 13
 Q9A523 PRELIMINARY; PRT; 666 AA.
 ID Q9A523
 AC Q9A523
 DT 01-JUN-2001 (Tremblrel. 17, Created)

```

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT Oligopeptide transporter, OPT family.
GN CC2646.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C. Felsblyum T.V. Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A.C., Stephens C., Madacki N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; A0005932; AAK24613.1; -.
DR PIR; A87577; A87577.
DR TIGR; CC2646; -.
DR InterPro; IPR004813; OPT fam.
DR InterPro; IPR004813; Tetrapept_transpt.
DR Pfam; PF03169; OPT; 1.
DR TIGRfams; TIGR00728; OPT_sfam; 1.
DR TIGRfams; TIGR00733; TIGR00733; 1.
KW Complete proteome.
SQ SEQUENCE 666 AA; 67569 MW; 1ED3FF286CA8B6C0 CRC64;

Query Match 9.9%; Score 88.5; DB 16; Length 666;
Best Local Similarity 32.5%; Pred. No. 7.1;
Matches 37; Conservative 14; Mismatches 48; Indels 15; Gaps 4;

QY 50 LGHSLGIPWAPISSCPSQALQAGCLSLQHSGLFYQGLQALQEGISPELGTLDLQD 109
DB 196 LGASGATGIGASS--SLALMGAGHLGITVGVAMFTGLFAWAILPILTLVTMPD 253

QY 110 VADFATTIQQ-QHEELG-----MAPALQP-TCGAMPAPAFASAFQRRAGG 150
DB 254 AATHALTVKRSQVRFLGAGVIGAAIWTAKLVGPIITSLGKSAFAAQAARKAGG 307

RESULT 14
ID Q91019 PRELIMINARY; PRT; 786 AA.
AC Q91019;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable sensor/response regulator hybrid.
GN PA2824.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wock G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

-!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
CC EMBL; AE004709; AAG06212.1; -.
DR PIR; F83292; F83292.
DR HSSP; P06143; IAB6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0000156; F:two-component sensor molecule activity; IEA.
DR GO; GO:0000155; F:two-component sensor perception; IEA.
DR GO; GO:0000160; F:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR PRINTS; PR00072; Response_reg; 1.
DR PRODOM; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW kinase; Phosphorylation; Sensory transduction; Transferase;
KW Complete proteome.
SQ SEQUENCE 786 AA; 85860 MW; 3B134513F3538F7C CRC64;

Query Match 9.9%; Score 88.5; DB 16; Length 786;
Best Local Similarity 29.2%; Pred. No. 8.6;
Matches 50; Conservative 19; Mismatches 49; Indels 53; Gaps 10;

QY 26 GDGAALQEKLC-ATYKLCHEPELVVLG--HSLGIPWAPISSCPSQALQAG-CLSGLHSG 81
DB 490 GLGLALTRKLCCEANQMGELTVESTVGLGSLFVGLPLAVSP-PLQALPLRGVIAQCSAN 548

QY 82 LFLYVQGLQALQEGISPE-----LGPTLDTLQDVLQVDFATTIQQMEELGMA 127
DB 549 -----SGLAQLLQTLWLPFWGLGLEYKRLTDDSLGHSUDVLISDCPCL-----MGLR 595

QY 128 PALQPTQGMAPAFASAFQRRAGGLVASHLQSPFL--EVSRYV--LRHLAQP 174
DB 596 PSI-----GTPILLVTAYGSLFLEPELARLRLSPLQLARP 629

RESULT 15
ID Q8RJY3 PRELIMINARY; PRT; 1931 AA.
AC Q8RJY3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Stid protein.
GN STID.
OS Stigmatella aurantiaca.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Cystobacteraceae; Stigmatella.
OX NCBI_TaxID=41;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SG al5;
RA Gaitatzis N., Silakowski B., Kunze B., Nordsiek G., Blocker H.,
RA Hofle G., Muller R.;
RT "The biosynthesis of the aromatic myxobacterial electron transport
RT inhibitor stigmatellin is directed by a novel type of modular
RT polyketide synthase.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ421825; CAD19088.1; -.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.

```

This Page Blank (uspto)



```

GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPRO01227; AC:trans.
InterPro; IPRO00794; Ketoacyl_synth.
InterPro; IPRO01601; Methyltransf.
InterPro; IPRO06163; Pp bind.
InterPro; IPRO00051; SAM bind.
InterPro; IPRO02155; Thiolase.
Pfam; PF00698; Acyl_transf; 1.
Pfam; PF00103; ketoacyl_synth; 1.
Pfam; PF02801; ketoacyl_synth_C; 1.
Pfam; PF00550; pp-binding; 1.
PROSITE; PS00075; ACP DOMAIN; 1.
PROSITE; PS00606; B KETOACYL SYNTHASE; 1.
PROSITE; PS00098; THIOLASE 1; 1.
Phosphopantetheine; Transferase.
SEQUENCE 1931 AA; 208260 MW; 6DEAAQF496A9A84F CRC64;

Query Match          9.98; Score 88.5; DB 2; Length 1931;
Best Local Similarity 25.3%; Pred. No. 25;
Matches 41; Conservative 24; Mismatches 48; Indels 49; Gaps 6;

QY      6  ASSLPQSFLLKCLQEVRKIQGDGAALQKELCATYK---LCHPEELVLGHSLGIPWAPLS 62
Db      734 ASNGPRSTVL-----SGDPAALEQLVTSRRQEVFCRPVDVDVASHS----- 775
QY      63  SCPQQAQLAGCLSQLHSGFLVQGLLQALEGISPELGTPLDTLQDVADFATTIQQOME 122
Db      776 -----PQMEPLLEPERGLAVLPRAAAVFFVSTVLDVLGRDLDSYWAENL----- 824
QY      123  ELGMAPALQPTQGGAMPAPASAFORRAGGVLVASHLQSFLEVS 164
Db      925 ---RSPVL-----FFQSLQR-----LIAAGHELFLFEVS 849

```

Search completed: October 6, 2004, 16:06:34
Job time : 121 secs


```

Query Match          49.6%; Score 89.2; DB 1; Length 642;
Best Local Similarity 76.8%; Pred. No. 4.8e-20;
Matches 109; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTTCATGAGTATCAGC 60

QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGGA 120
DB 61 ATGTTTTCGGCAACCGCCTCTGCAGCTGGCCGCCACCATCAGATTACTGGCAAAATTTGGACTGACGGG 120

QY 121 AGGACTCCGTTAGTCCAGCA 142
DB 121 GCGGGACAGTAACGAGTCA 142

RESULT 2
US-08-104-445-1
; Sequence 1, Application 08/104445
; Patent No. 530633
; GENERAL INFORMATION:
; APPLICANT: GOTTSCHALK, MICHAEL
; APPLICANT: SCHUSTER, ERWIN
; APPLICANT: SPROESSLER, BRUNO
; TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS
; TITLE OF INVENTION: PRODUCTION, BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT
; TITLE OF INVENTION: ENCODING A XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT,
; TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 08/104,445
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 530633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 583-179-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-104-445-1

Query Match          49.6%; Score 89.2; DB 1; Length 1413;
Best Local Similarity 76.8%; Pred. No. 6.7e-20;
Matches 109; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTTCATGAGTATCAGC 60
DB 506 ATGTTTAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTTCATGAGTATCAGC 565
QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGGA 120

```

```

DB 566 ATGTTTTCGGCAACCGCCTCTGCAGCTGGCCGCCACAGATTACTGGCAAAATTTGGACTGACGGG 625
QY 121 AGGACTCCGTTAGTCCAGCA 142
DB 626 GCGGGACAGTAACGAGTCA 647

RESULT 3
US-09-570-856B-2
; Sequence 2, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Bacillus circulans
US-09-570-856B-2

Query Match          43.9%; Score 79; DB 4; Length 1349;
Best Local Similarity 79.0%; Pred. No. 1.6e-16;
Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTTCATGAGTATCAGC 60
DB 392 ATGTTTAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTTCATGAGTATCAGC 451
QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGG 119
DB 452 TTGTTTTCGGCAACCGCCTCTGCAGCTAGCAGACTACTGGCAAAATTTGGACTGATGG 510

RESULT 4
US-08-575-964-2
; Sequence 2, Application US/08575964
; Patent No. 5736384
; GENERAL INFORMATION:
; APPLICANT: Fukunaga, No. 5736384uyuki
; APPLICANT: Iwasaki, Yuji
; APPLICANT: Kono, Satoko
; APPLICANT: Kita, Yukio
; APPLICANT: Izumi, Yoshiya
; TITLE OF INVENTION: THERMOSTABLE XYLANASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,964
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347

```


Patent No. 6022535
GENERAL INFORMATION:
APPLICANT: Bennett, Dennis A.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-318-178

Query Match 28.1%; Score 50.6; DB 3; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 124 ACTCGTTAGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
Db 7 ACACCATAGGACCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 63

RESULT 8
US-08-468-609A-177
Sequence 177, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maïre H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKeam, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-609A-177

Query Match 28.1%; Score 50.6; DB 3; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 124 ACTCGTTAGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
Db 7 ACACCATAGGACCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 63

RESULT 9
US-08-468-609A-178
Sequence 178, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maïre H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKeam, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-609A-178

Query Match 28.1%; Score 50.6; DB 3; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTTAGAG 180
DB 7 ACACCATAGGACCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTTAGAG 63

RESULT 10

US-08-446-872A-177
Sequence 177, Application US/08446872A
Patent No. 6361977

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Mairé H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 737-6986

TELEFAX: (314) 737-6972

INFORMATION FOR SEQ ID NO: 177:

SEQUENCE CHARACTERISTICS:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-446-872A-177

Query Match 28.1%; Score 50.6; DB 4; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTTAGAG 180

DB 7 ACACCATAGGACCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTTAGAG 63

RESULT 11

US-08-446-872A-178
Sequence 178, Application US/08446872A
Patent No. 6361977

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Mairé H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 737-6986

TELEFAX: (314) 737-6972

INFORMATION FOR SEQ ID NO: 178:

LENGTH: 546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-446-872A-178

Query Match 28.1%; Score 50.6; DB 4; Length 546;

Best Local Similarity 93.0%; Pred. No. 2.7e-07;

Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTTAGAG 180

DB 7 ACACCATAGGACCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTTAGAG 63

RESULT 12

US-08-762-227A-177

Sequence 177, Application US/08762227A

Patent No. 6436387

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maïre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Ollins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/445,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-8881
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 177:
US-08-762-227A-177
Query Match 28.1%; Score 50.6; DB 4; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
124 ACTCCGTTAGTCCAGCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTCTAG 180
7 ACACATTAGCCCTGCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTCTAG 63
RESULT 13
US-08-762-227A-178
; Sequence 178, Application US/08762227A
; Patent No. 6436387
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Maïre H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Ollins, Peter O.

; INFORMATION FOR SEQ ID NO: 177:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-177

Query Match 28.1%; Score 50.6; DB 5; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
|||
DB 7 ACACCATAGGCGCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 63

RESULT 15

PCT-US95-01185-178
; Sequence 178, Application PC/TUS9501185

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01185
; FILING DATE: 02-FEB-1995

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192325
; FILING DATE: 14-FEB-1994

; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-178

Query Match 28.1%; Score 50.6; DB 5; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
|||
DB 7 ACACCATAGGCGCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 63

Search completed: October 9, 2004, 04:24:24
Job time : 28.6529 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 21:19:03 ; Search time 136.728 Seconds
(without alignments)
5592.665 Million cell updates/sec

Title: US-10-009-792C-26

Perfect score: 180

Sequence: 1 atgtttaagttaaagaagaa.....tccgtgctaagtgcttag 180

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB ID	Description
1	180	100.0	AAD19775	Aad19775 Human hg-
2	89.2	49.6	AQ56052	Aq56052 Sequence
3	89.2	49.6	AAQ66480	Aa66480 Sequence
4	87.6	48.7	AAA47153	Aaa47153 DNA encod
5	86	47.8	AAD19774	Aad19774 Human hg-
6	79.6	44.2	AA47157	Aaa47157 DNA encod
7	79.6	44.2	AAA47155	Aaa47155 DNA encod
8	79.6	44.2	AAA47156	Aaa47156 DNA encod
9	79	43.9	AA47154	Aaa47154 DNA encod
10	79	43.9	AAQ13814	Aaa13814 DNA encod
11	79	43.9	ADC27538	Adc27538 Bacillus
12	79	43.9	AAAC8889	Aac88889 Bacillus
13	79	43.9	AA148894	Aal48894 B circula
14	52	28.9	AA171848	Aai71848 Recombina
15	50.6	28.1	AAQ97205	Aaq97205 PMON13010
16	50.6	28.1	AAQ97206	Aaq97206 PMON13499
17	50.6	28.1	AAA03772	Aaa03772 Human G-C
18	50.6	28.1	AAA03773	Aaa03773 Human G-C
19	50.6	28.1	ABX00088	Abx00088 Human int
20	50.6	28.1	ABX00087	Abx00087 Human int
21	50.6	28.1	AAW70029	Aan70029 Mature na
22	50.6	28.1	AAQ97167	Aaq97167 PMON13023
23	50.6	28.1	AAA03721	Aaa03721 Human int

24	50.6	28.1	906	6	ABX00010	Abx00010 Human int
25	50.6	28.1	921	2	AAQ97198	Aaq97198 PMON13066
26	50.6	28.1	921	2	AAQ97186	Aaq97186 PMON13026
27	50.6	28.1	921	2	AAQ97189	Aaq97189 PMON13043
28	50.6	28.1	921	2	AAQ97192	Aaq97192 PMON13151
29	50.6	28.1	921	3	AAA03746	Aaa03746 Human int
30	50.6	28.1	921	3	AAA03752	Aaa03752 Human int
31	50.6	28.1	921	3	AAA03740	Aaa03740 Human int
32	50.6	28.1	921	3	AAA03743	Aaa03743 Human int
33	50.6	28.1	921	6	ABX00029	Abx00029 Human int
34	50.6	28.1	921	6	ABX00035	Abx00035 Human int
35	50.6	28.1	921	6	ABX00032	Abx00032 Human int
36	50.6	28.1	921	6	ABX00041	Abx00041 Human int
37	50.6	28.1	966	2	AAQ97185	Aaq97185 PMON13060
38	50.6	28.1	966	2	AAQ97191	Aaq97191 PMON13045
39	50.6	28.1	966	2	AAQ97184	Aaq97184 PMON13058
40	50.6	28.1	966	2	AAQ97187	Aaq97187 PMON13063
41	50.6	28.1	966	2	AAQ97193	Aaq97193 PMON13152
42	50.6	28.1	966	2	AAQ97182	Aaq97182 PMON13034
43	50.6	28.1	966	3	AAA03741	Aaa03741 Human int
44	50.6	28.1	966	3	AAA03745	Aaa03745 Human int
45	50.6	28.1	966	3	AAA03736	Aaa03736 Human int

ALIGNMENTS

RESULT 1

AAD19775

ID AAD19775 standard; DNA; 180 BP.

XX

AC AAD19775;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human hg-CSF DNA 5' end inserted into plasmid pTHSCSFmlI.

XX

KW Human; granulocyte colony stimulating factor; hg-CSF; protease;

KW Factor Xa; Kanamycin resistance; endoxylanase signal peptide; ds.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT CDS

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

PT Recombinant plasmid vector comprising an endoxylanase signal sequence,
 CC human granulocyte colony stimulating factor gene and other components,
 PT when transformed into microorganism useful for preparing the colony
 PT stimulating factor.

XX Claim 3; Fig 12; 50pp; English.

CC The invention relates to an Escherichia coli producing and secreting
 CC human granulocyte colony stimulating factor (hG-CSF), more specifically,
 CC to a recombinant plasmid constructed to express secretory hG-CSF in E.
 CC coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a
 CC process for preparing hG-CSF using the transformed hG-CSF. The
 CC recombinant plasmid vector comprises of a kanamycin resistance gene, a
 CC promoter, an endoxylanase signal sequence, a nucleotide sequence coding
 CC for an oligopeptide consisting of 13 amino acids including 6 consecutive
 CC histidine residues and a hG-CSF. E.coli transformed with recombinant
 CC plasmid vector is useful for preparing hG-CSF. The method comprises
 CC culturing the microorganism to obtain a hG-CSF fusion protein and
 CC treating the fusion protein with a protease preferably Factor Xa, to
 CC obtain a hG-CSF where the fusion protein is obtained from the culture by
 CC employing Ni-column. The present sequence is a DNA encoding human hG-CSF
 CC N-terminal region inserted into plasmid pTHSCSFmlI

XX Sequence 180 BP; 44 A; 50 C; 40 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 180; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.8e-50;

Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60
 QY 61 ATGTTTCTGCACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGGA 120
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 61 ATGTTTCTGCACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGGA 120
 QY 121 AGGACTCCGTTAGTCTCAGCAGCTCCCTGCCCGCAGAGCTTCTGCTCAAGTCTTAGAG 180
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 121 AGGACTCCGTTAGTCTCAGCAGCTCCCTGCCCGCAGAGCTTCTGCTCAAGTCTTAGAG 180

RESULT 2

AAQ56052

ID AAQ56052 standard; DNA; 642 BP.

XX AAQ56052;

AC AAQ56052;

DT 25-MAR-2003 (revised)

DT 10-AUG-1994 (first entry)

XX Sequence encoding xylanase.

DE Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;

XX bread; pastry; ss.

KW Bacillus subtilis.

OS DE4226528-A1.

XX DB4226528-A1.

XX 17-FEB-1994.

XX 11-AUG-1992; 92DE-04226528.

XX 11-AUG-1992; 92DE-04226528.

XX (ROHG) ROEHM GMBH.

XX Gottschalk M, Sproessler B, Schuster E;

XX WPI; 1994-056089/08.

XX P-PSDB; AAR47200.

XX Query Match 99.6%; Score 89.2; DB 2; Length 1413;

PT New xylanase obtd. from Bacillus subtilis - useful in baking agents for
 PT increased vol. of baking prods.

XX Claim 4; Page 10; 11pp; German.

XX The modified xylanase is used as a baking agent, preferably for yeast

CC pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 642 BP; 191 A; 122 C; 166 G; 163 T; 0 U; 0 Other;

QY Query Match 49.6%; Score 89.2; DB 2; Length 642;

Best Local Similarity 76.8%; Pred. No. 1.2e-19;

Matches 109; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60

DB 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60

QY 61 ATGTTTCTGCACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGGA 120

DB 61 ATGTTTCTGCACCGCCTCTGCAGCTGGCCGCCACCATCACCATCACCATATCGAGGGA 120

QY 121 AGGACTCCGTTAGTCTCAGCAGCTCCCTGCCCGCAGAGCTTTCATGATATCAGC 142

DB 121 GCGCGGACAGTAACGGCAGTCA 142

RESULT 3

AAQ66480

ID AAQ66480 standard; DNA; 1413 BP.

XX AAQ66480;

AC AAQ66480;

DT 25-MAR-2003 (revised)

DT 10-AUG-1994 (first entry)

XX Sequence comprising xylanase coding sequence.

DE Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;

XX bread; pastry; ss.

KW Bacillus subtilis.

OS DE4226528-A1.

XX DE4226528-A1.

XX 17-FEB-1994.

XX 11-AUG-1992; 92DE-04226528.

XX 11-AUG-1992; 92DE-04226528.

XX (ROHG) ROEHM GMBH.

XX Gottschalk M, Sproessler B, Schuster E;

XX WPI; 1994-058089/08.

XX New xylanase obtd. from Bacillus subtilis - useful in baking agents for

CC increased vol. of baking prods.

XX Example 4; Page 9; 11pp; German.

XX The modified xylanase is used as a baking agent, preferably for yeast

CC pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 1413 BP; 408 A; 280 C; 317 G; 408 T; 0 U; 0 Other;

QY Query Match 49.6%; Score 89.2; DB 2; Length 1413;

Best Local Similarity 76.8%; Pred. No. 1.7e-19;
Matches 109; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGTTTAAAGTTTAAAAAGAAATTCCTAGTGGGATTAAAGCGAGCTTTTCATGAGTATCAGC 60
Db 506 ATGTTTAAAGTTTAAAAAGAAATTCCTAGTGGGATTAAAGCGAGCTTTTCATGAGTATCAGC 565

QY 61 ATGTTTTCGCAACGGCTCTGCAGCTGGCCGCGCACCATCACCATCACCATATCGAGGA 120
Db 566 ATGTTTTCGCAACGGCTCTGCAGCTGGCCGCGCACCATCACCATCACCATATCGAGGA 625

QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 626 GCGGGACAGTAACGCAGTCA 647

RESULT 4
AAA47153
ID AAA47153 standard; DNA; 642 BP.
XX
AC AAA47153;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding a bacterial endo-beta-1,4-xylanase protein.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
KW dough; dough preparation; ss.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT CDS 1..642
FT /*tag= a
FT /product= "xylanase"
XX
PN WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX
PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
XX
PA (DANI-) DANISCO AS.
XX
PI Sibbesen O, Sorensen JF;
XX
XX WPI; 2000-465744/40.
DR P-PSDB; AAY93751.
XX
PT Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
XX
PS Disclosure; Page 107; 112pp; English.
XX
CC The present sequence encodes an endo-beta-1,4-xylanase. The specification
CC also describes an endo-beta-1,4-xylanase inhibitor, which is obtained
CC from wheat flour. The specification also describes a mutant xylanase
CC protein. The xylanase is useful for preparing a foodstuff, preferably a
CC bakery product or a substance (e.g. a dough) for making the bakery
CC product. Wild type xylanase or mutant xylanase is useful for preparing a
CC dough that is less sticky than a dough comprising a fungal xylanase. The
CC xylanase inhibitor is useful for screening high degree resistance
CC xylanases for dough preparation. The xylanase is also useful for
CC preparing a non-sticky dough. A combination of xylanase and the inhibitor
CC is useful for calibrating and/or determining the quantity of inhibitor in
CC a wheat flour sample
XX
SQ Sequence 642 BP; 192 A; 122 C; 164 G; 164 T; 0 U; 0 Other;

Query Match 48.7%; Score 87.6; DB 3; Length 642;
Best Local Similarity 76.1%; Pred. No. 4.2e-19;
Matches 108; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGTTTAAAGTTTAAAAAGAAATTCCTAGTGGGATTAAAGCGAGCTTTTCATGAGTATCAGC 60
Db 1 ATGTTTAAAGTTTAAAAAGAAATTCCTAGTGGGATTAAAGCGAGCTTTTCATGAGTATCAGC 60

QY 61 ATGTTTTCGCAACGGCTCTGCAGCTGGCCGCGCACCATCACCATCACCATATCGAGGA 120
Db 61 ATGTTTTCGCAACGGCTCTGCAGCTGGCCGCGCACCATCACCATCACCATATCGAGGA 120

QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 121 GCGGGACAGTAACGCAGTCA 142

RESULT 5
AAD19774
ID AAD19774 standard; DNA; 135 BP.
XX
AC AAD19774;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human hg-CSF DNA 5' end inserted into plasmid pTrcSCSFml.
XX
KW Human; granulocyte colony stimulating factor; hg-CSF; protease;
KW Factor Xa; kanamycin resistance; endoxylanase signal peptide; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..135
FT /*tag= a
FT /product= "Human hg-CSF protein fragment"
FT /note= "CDS does not include stop codon"
FT /partial
FT sig_peptide 1..84
FT /*tag= b
FT mat_peptide 85..135
FT /*tag= c
FT /product= "Human mature hg-CSF protein fragment"
XX
PN WO200173081-A1.
XX
PD 04-OCT-2001.
XX
XX 31-MAR-2001; 2001WO-KR000549.
XX
PR 31-MAR-2000; 2000KR-00017052.
XX
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX
PI Lee S, Jeong K;
XX
XX WPI; 2001-616523/71.
DR P-PSDB; AAE12156.
XX
XX Recombinant plasmid vector comprising an endoxylanase signal sequence,
XX human granulocyte colony stimulating factor gene and other components,
XX when transformed into microorganism useful for preparing the colony
XX stimulating factor.
XX
PS Example 4; Fig 9; 50pp; English.
XX
CC The invention relates to an Escherichia coli producing and secreting
CC human granulocyte colony stimulating factor (hg-CSF), more specifically,
CC to a recombinant plasmid constructed to express secretory hg-CSF in E.
CC coli, an E. coli transformed with that plasmid to secrete hg-CSF, and a
CC process for preparing hg-CSF using the transformed hg-CSF. The
CC recombinant plasmid vector comprises of a kanamycin resistance gene, a
CC promoter, an endoxylanase signal sequence, a nucleotide sequence coding

CC for an oligopeptide consisting of 13 amino acids including 6 consecutive
 CC histidine residues and a hg-CSF. E.coli transformed with recombinant
 CC plasmid vector is useful for preparing hg-CSF. The method comprises
 CC culturing the microorganism to obtain a hg-CSF fusion protein and
 CC treating the fusion protein with a protease preferably Factor xa, to
 CC obtain a hg-CSF, where the fusion protein is obtained from the culture by
 CC employing Ni-column. The present sequence is a DNA encoding human hg-CSF
 CC N-terminal region inserted into plasmid pRCSFm11
 XX
 XX Sequence 135 BP; 32 A; 36 C; 28 G; 39 T; 0 U; 0 Other;

Query Match 47.8%; Score 86; DB 4; Length 135;
 Best Local Similarity 77.6%; Pred. No. 7.8e-19;
 Matches 135; Conservative 0; Mismatches 0; Indels 39; Gaps 1;
 QY 1 ATGTTTAAAGTTTAAAGAAATCTTGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
 DB 1 ATGTTTAAAGTTTAAAGAAATCTTGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
 QY 61 ATGTTTCTGCACCGCTCTGCAGCTGCGCCGCCACCATCACCATATCGAGGGA 120
 DB 61 ATGTTTCTGCACCGCTCTGCAGCTGCGCCGCCACCATCACCATATCGAGGGA 120
 QY 121 AGGACTCCGTTAGTCCAGCAGCTCCCTGCGCCGAGCTTCTGCTCAAGTGC 174
 DB 85 ---ACTCCGTTAGTCCAGCAGCTCCCTGCGCCGAGCTTCTGCTCAAGTGC 135

RESULT 6
 AAA47157
 ID AAA47157 standard; DNA; 642 BP.
 AC AAA47157;
 DT 03-OCT-2000 (first entry)
 XX DNA encoding a bacterial endo-beta-1,4-xylanase mutant XM3.
 DE
 XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
 KW dough; dough preparation; ss.
 XX
 XX Synthetic.
 OS Bacillus subtilis.
 XX
 XX Key Location/Qualifiers
 FH 1..642
 FT /*tag= a
 FT /product= "xylanase mutant"
 XX
 XX WO200039289-A2.
 XX
 XX 06-JUL-2000.
 XX
 XX 17-DEC-1999; 99WO-IB002071.
 XX
 XX 23-DEC-1998; 98GB-00028599.
 PR 06-APR-1999; 99GB-00007805.
 PR 15-APR-1999; 99GB-00008645.
 XX
 XX (DANI-) DANISCO AS.
 XX
 XX Sibbesen O, Sorensen JF;
 XX
 XX WPI; 2000-465744/40.
 DR P-PSDB; AAY93755.
 XX
 XX Mutant xylanase protein identified using xylanase inhibitor useful for
 PT preparing non-sticky dough for bakery products.
 XX
 XX Claim 3; Page 111; 112pp; English.

XX The present sequence encodes a mutant endo-beta-1,4-xylanase. The
 CC specification also describes an endo-beta-1,4-xylanase inhibitor, which

CC is obtained from wheat flour. The specification also describes a mutant
 CC xylanase protein. The xylanase is useful for preparing a foodstuff,
 CC preferably a bakery product or a substance (e.g. a dough) for making the
 CC bakery product. Wild type xylanase or mutant xylanase is useful for
 CC preparing a dough that is less sticky than a dough comprising a fungal
 CC xylanase. The xylanase inhibitor is useful for screening high degree
 CC resistance xylanases for dough preparation. The xylanase is also useful
 CC for preparing a non-sticky dough. A combination of xylanase and the
 CC inhibitor is useful for calibrating and/or determining the quantity of
 CC inhibitor in a wheat flour sample
 XX
 XX Sequence 642 BP; 192 A; 110 C; 162 G; 178 T; 0 U; 0 Other;

Query Match 44.2%; Score 79.6; DB 3; Length 642;
 Best Local Similarity 72.5%; Pred. No. 2.1e-16;
 Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
 QY 1 ATGTTTAAAGTTTAAAGAAATCTTGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
 DB 1 ATGTTTAAAGTTTAAAGAAATCTTGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
 QY 61 ATGTTTCTGCACCGCTCTGCAGCTGCGCCGCCACCATCACCATATCGAGGGA 120
 DB 61 TTGTTTTCGGCAACCGCTCTGCAGCTAGCAGACTACTGGCAAAATTTGGACTGATGGG 120
 QY 121 AGGACTCCGTTAGTCCAGCCA 142
 DB 121 GGCGGTACCGTAAACGCTGTCA 142

RESULT 7
 AAA47155
 ID AAA47155 standard; DNA; 642 BP.
 AC AAA47155;
 DT 03-OCT-2000 (first entry)
 XX DNA encoding a bacterial endo-beta-1,4-xylanase mutant XM1.
 DE
 XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
 KW dough; dough preparation; ss.
 XX
 XX Synthetic.
 OS Bacillus subtilis.
 XX
 XX Key Location/Qualifiers
 FH 1..642
 FT /*tag= a
 FT /product= "xylanase mutant"
 XX
 XX WO200039289-A2.
 XX
 XX 06-JUL-2000.
 XX
 XX 17-DEC-1999; 99WO-IB002071.
 XX
 XX 23-DEC-1998; 98GB-00028599.
 PR 06-APR-1999; 99GB-00007805.
 PR 15-APR-1999; 99GB-00008645.
 XX
 XX (DANI-) DANISCO AS.
 XX
 XX Sibbesen O, Sorensen JF;
 XX
 XX WPI; 2000-465744/40.
 DR P-PSDB; AAY93753.
 XX
 XX Mutant xylanase protein identified using xylanase inhibitor useful for
 PT preparing non-sticky dough for bakery products.
 XX
 XX Claim 3; Page 109; 112pp; English.

This Page Blank (uspto)

XX Sequence 546 BP; 95 A; 189 C; 157 G; 105 T; 0 U; 0 Other;
SQ
Query Match 28.1%; Score 50.6; DB 2; Length 546;
Best Local Similarity 93.0%; Pred. No. 1.2e-06;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 124 ACTCGTTAGTCCAGCCAGCTCCCTGCCCCCAGAGCTTCCTGCTCAAGTGTAGAG 180
Db 7 ACACCATAGGACCTGCCAGCTCCCTGCCCCCAGAGCTTCCTGCTCAAGTGTAGAG 63

Search completed: October 9, 2004, 02:07:18
Job time : 138.728 secs

CC protein has been modified to exhibit enhanced thermophilicity,
 CC alkalophilicity, or thermostability relative to naturally occurring B.
 CC circular xylanase, and has at least 5 amino acid substitutions. A
 CC bleaching agent comprising a modified xylanase is useful for bleaching
 CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
 CC clarifying juice and wine, extracting coffee, plant oils and starch,
 CC producing food thickeners, altering texture in bakery products, e.g.
 CC improving the quality of dough, helping bread to rise and processing of
 CC wheat and corn for starch production, use as animal food additives to aid
 CC in the digestibility of feedstuffs and in the washing of super precision
 CC devices and semiconductors. The present sequence is a coding sequence of
 CC a xylanase protein described in the exemplification of the invention
 XX
 XX Sequence 1349 BP; 396 A; 232 C; 312 G; 409 T; 0 U; 0 Other;

Query Match 43.9%; Score 79; DB 6; Length 1349;
 Best Local Similarity 79.0%; Pred. No. 4.5e-16;
 Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 ATGTTTAAAGTTTAAAGAAATTCCTTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
 Db 392 ATGTTTAAAGTTTAAAGAAATTCCTTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 451
 QY 61 ATGTTTTCGCAACCGCTTCGACCTGGCGCGACCATCACCATCACCATATCGAGG 119
 Db 452 TTGTTTTCGCAACCGCTTCGACCTGGCGCGACCATCACCATCACCATATCGAGG 510

RESULT 14
 AA171848
 ID AA171848 standard; cDNA; 644 BP.
 AC AA171848;
 XX
 XX 07-JAN-2002 (first entry)
 XX Recombinant human granulocyte colony stimulating factor cDNA.
 XX Human; granulocyte colony stimulating factor; rhG-CSF; recombinant; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 94..621
 FT /*tag= a
 FT /product= "rhG-CSF"

XX
 XX CN1167150-A.
 XX 10-DEC-1997.
 XX 05-JUN-1996; 96CN-00106418.
 XX 05-JUN-1996; 96CN-00106418.
 XX (JIUYU-) JIUYUAN GENE ENG CO LTD HANGZHOU.
 XX Su Y, Kong T, Wang C;
 XX WPI; 2001-590346/67.
 XX P-PSDB; AAM51536.
 XX Production of recombinant human granulocyte colony stimulation factor.
 XX Disclosure; Page 8 (disclosure); 15pp; Chinese.

XX The invention relates to a method for producing recombinant human
 CC granulocyte colony stimulating factor (rhG-CSF). The method includes the
 CC following steps: (a) reverse transcription-polymerase chain reaction of
 CC the human granulocyte colony stimulating factor gene; (b) transforming
 CC Escherichia coli; (c) renaturation of protein by hollow fibre
 CC ultrafiltration dialysis; (d) passing the renatured protein through ion
 CC exchange chromatography, hydrophobic chromatography and molecular sieve

CC chromatography which are combined together sequentially; and (e)
 CC purifying so to obtain a high yield of high-purity medicinal rhG-CSF
 CC protein. The present sequence encodes rhG-CSF
 XX
 XX Sequence 644 BP; 128 A; 216 C; 172 G; 128 T; 0 U; 0 Other;
 Query Match 28.9%; Score 52; DB 5; Length 644;
 Best Local Similarity 91.7%; Pred. No. 4.2e-07;
 Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 121 AGGATTCCTAGTCCAGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGCTTAGAG 180
 Db 94 ATGACACCATTAGGCGCTCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGCTTAGAG 153

RESULT 15
 AAQ97205
 ID AAQ97205 standard; DNA; 546 BP.

XX
 XX AAQ97205;
 XX 25-AUG-1999 (first entry)
 XX pMON13010 DNA sequence.
 XX Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
 XX mutant; mutein; fusion protein; linker; ss.
 XX Synthetic.
 XX Homo sapiens.
 XX WO9521254-A1.
 XX 10-AUG-1995.
 XX 02-FEB-1995; 95WO-US001185.
 XX 04-FEB-1994; 94US-00192325.
 XX (SEAR) SEARLE & CO G D.
 XX Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 XX Klein BK, McKearn JP, Olin PO, Paik K, Thomas JW;
 XX WPI; 1995-283774/37.
 XX P-PSDB; AAR79336.
 XX Fusion proteins comprising a human interleukin-3 variant, a linker and
 XX interleukin-3, a variant or a colony stimulating factor - useful to
 XX increase haematopoietic cell prodn. in a mammal.

Example 15; Page 183-184; 447pp; English.

XX A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
 CC R1-R2, R1-L-R1 or R1-L-R1, where R1 is a mutant or variant of human
 CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
 CC including cytokines, lymphokine, interleukin, haematopoietic growth factor
 CC or IL-3 variant, and L is a linker. Generic sequences are described in
 CC AA03235 - AA03242, and specifically claimed examples are shown in
 CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
 CC recombinant DNA techniques. Specifically claimed examples of DNA
 CC sequences which encode these proteins are shown in AAQ97167-Q97204 and
 CC AAQ97222-Q97227. The fusion protein is used to increase haematopoietic
 CC cell production. It is also useful as an IL-3 antagonist or as a discrete
 CC antigenic fragment for production of antibodies useful in immunoassays
 CC and immunotherapy. Antagonists are used to block the growth of certain
 CC cancer cells and in treatment of asthma. The fusion protein can also be
 CC used to stimulate bone marrow and blood cell activation and growth in
 CC vitro before infusion; and to treat diseases characterised by decreased
 CC levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the
 CC haematopoietic system. The protein has the usual activity of both its
 CC component proteins, but may have increased synergistic activity and
 CC reduced undesired side effects

PI Bentzien JM;
 XX WPI; 2000-579800/56.
 DR P-PSDB; AAB48530.
 XX
 XX Non naturally occurring XA protein with enhanced thermophilicity.
 PT alkalophilicity or thermostability relative to the naturally occurring
 PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
 XX
 PS Disclosure; Fig 1C; 114pp; English.
 XX
 CC The present sequence is given in a specification relating to non
 CC naturally occurring xylanase activity (XA) proteins. The XA proteins
 CC comprise an amino acid sequence less than 97% identical to a naturally
 CC occurring Bacillus circulans xylanase. They are modified to exhibit
 CC enhanced thermophilicity, alkalophilicity or thermostability relative to
 CC the naturally occurring B. circulans xylanase. They may be used as the
 CC active compound in a bleaching agent which is used for bleaching pulp
 XX
 SQ Sequence 1349 BP; 396 A; 232 C; 312 G; 409 T; 0 U; 0 Other;
 Query Match 43.9%; Score 79; DB 3; Length 1349;
 Best Local Similarity 79.0%; Pred. No. 4.5e-16;
 Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 ATGTTTAACTTTAAAGAAATTTCTAGTGGGATTAAACGGCAGCTTTTATGATATCAGC 60
 Db 392 ATGTTTAACTTTAAAGAAATTTCTAGTGGGATTAAACGGCAGCTTTTATGATATCAGC 451
 QY 61 ATGTTTTCGCAACCGCTCTGCAGTGGCCGCCACCATCACCATATCGAGGG 119
 Db 452 TTGTTTTCGCAACCGCTCTGCAGTGGCCGCCACCATCACCATATCGAGGG 510
 RESULT 13
 AAL48894
 ID AAL48894 standard; DNA; 1349 BP.
 XX
 AC AAL48894;
 XX 24-OCT-2002 (first entry)
 DT B circulans xylanase coding sequence.
 DE
 XX Xylanase activity; enzymes; thermostable; xylanase; pulp bleaching;
 KW liquid clarification; coffee extraction; plant oil extraction; gene;
 KW starch extraction; food thickener; animal food additive; mutant; ds.
 XX
 OS Bacillus circulans.
 XX
 PN WO200238746-A2.
 XX
 PD 16-MAY-2002.
 XX
 XX 09-NOV-2001; 2001WO-US048018.
 PF
 XX 10-NOV-2000; 2000US-00710050.
 PR
 XX (XENC-) XENCOR INC.
 PA
 XX Bentzien J, Dahiyat B;
 PI
 XX WPI; 2002-608200/65.
 DR
 XX Novel xylanase activity protein, useful in bleaching process of pulp and
 PT in food and animal feed industry, has enhanced thermostability and
 PT alkalophilicity.
 XX
 PS Disclosure; Fig 1C; 121pp; English.
 XX
 CC The present invention relates to a non-naturally occurring xylanase
 CC activity (XA) protein comprising an amino acid sequence less than 97%
 CC identical to a naturally occurring Bacillus circulans xylanase, where the

DR P-PSDB; ABC27541, ABC27530.
 XX
 XX Novel variant xylanase polypeptide having altered sensitivity to a
 PT xylanase inhibitor and altered thermostability as compared with a
 PT parent xylanase enzyme, useful in baking, processing cereals, starch
 PT production.
 XX
 PS Example 2; Page 38; 63pp; English.
 XX
 XX This invention relates to a novel variant xylanase protein or its
 CC fragment having xylanase activity. The variants have one or more amino
 CC acid modifications so that the protein or fragment has an altered
 CC sensitivity to a xylanase inhibitor and has an altered thermostability
 CC as compared with a parent xylanase enzyme. The variant xylanases of the
 CC invention are useful for degrading or modifying a plant cell wall, and
 CC for processing cereals, starch production, in processing wood, and enhancing
 CC the bleaching of wood pulp. They may also be useful for a variety of
 CC applications such as animal feed, flour separation (wetmilling) and paper
 CC and pulp production. In addition, they may also be useful for preparing a
 CC flour dough. The enzymes of the invention may alter or reduce the
 CC viscosity derived from the presence of hemicellulose or arabinoxylan in a
 CC solution or system comprising plant cell wall material, and for modifying
 CC food and/or feed supplement comprising xylan. Use of the variant
 CC xylanases in baking processes improves the properties of flour based
 CC doughs and products made from the doughs. The baked products have highly
 CC desirable characteristics with respect to blood volume, crumb structure
 CC and appearance and additionally have an extended shelf-life. The enzymes
 CC of the invention have reduced thermostability and inhibitor
 CC sensitivity, which allows a reduction in the amount of xylanase required
 CC for animal feed, starch production and baking. The present sequence is
 CC the cDNA sequence which encodes the wild-type Bacillus subtilis xylanase
 CC which was used to create the variant xylanases of the invention.
 XX
 SQ Sequence 645 BP; 192 A; 111 C; 163 G; 179 T; 0 U; 0 Other;
 Query Match 43.9%; Score 79; DB 9; Length 645;
 Best Local Similarity 79.0%; Pred. No. 3.4e-16;
 Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 ATGTTTAACTTTAAAGAAATTTCTAGTGGGATTAAACGGCAGCTTTTATGATATCAGC 60
 Db 4 ATGTTTAACTTTAAAGAAATTTCTAGTGGGATTAAACGGCAGCTTTTATGATATCAGC 63
 QY 61 ATGTTTTCGCAACCGCTCTGCAGTGGCCGCCACCATCACCATATCGAGGG 119
 Db 64 TTGTTTTCGCAACCGCTCTGCAGTGGCCGCCACCATCACCATATCGAGGG 122
 RESULT 12
 AAC88889
 ID AAC88889 standard; DNA; 1349 BP.
 XX
 AC AAC88889;
 XX 05-MAR-2001 (first entry)
 DT Bacillus circulans xylanase DNA sequence.
 DE
 XX Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent; ds.
 KW
 XX Bacillus circulans.
 OS
 XX WO2000068396-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 12-MAY-2000; 2000WO-US013172.
 PF
 XX 12-MAY-1999; 99US-013714P.
 PR
 XX (XENC-) XENCOR INC.
 PA
 XX

XX
PS Disclosure; Page 108; 112pp; English.

XX
CC The present sequence encodes an endo-beta-1,4-xylanase. The specification
CC also describes an endo-beta-1,4-xylanase inhibitor, which is obtained
CC from wheat flour. The specification also describes a mutant xylanase
CC protein. The xylanase is useful for preparing a foodstuff, preferably a
CC bakery product or a substance (e.g. a dough) for making the bakery
CC product. Wild type xylanase or mutant xylanase is useful for preparing a
CC dough that is less sticky than a dough comprising a fungal xylanase. The
CC xylanase inhibitor is useful for screening high degree resistance
CC xylanases for dough preparation. The xylanase is also useful for
CC preparing a non-sticky dough. A combination of xylanase and the inhibitor
CC is useful for calibrating and/or determining the quantity of inhibitor in
CC a wheat flour sample

XX
SQ Sequence 642 BP; 191 A; 110 C; 163 G; 178 T; 0 U; 0 Other;

Query Match 43.9%; Score 79; DB 3; Length 642;
Best Local Similarity 79.0%; Pred. No. 3.4e-16;
Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60

QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGGCGCCGACCATCACCATCACCATATCGAGGG 119
DB 61 TTGTTTTCGGACACCGCCTCTGCAGCTAGCAGACTACTGGCAAAATTCGACTGATGG 119

RESULT 10
AA13814
ID AA13814 standard; DNA; 645 BP.
AC AA13814;
XX
DT 18-DEC-2001 (first entry)
XX
DE DNA encoding Bacillus subtilis xylanase.
KW Xylanase; plant cell wall; baking; cereal; starch production; wood;
KW wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; ds.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT CDS 98..645
FT /*tag= a
FT /*product= "xylanase"

XX
PN WO200166711-A1.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-IB000426.
XX
PR 08-MAR-2000; 2000GB-00005585.
XX
PR 27-JUN-2000; 2000GB-00015751.
XX
PA (DANI-) DANISCO AS.
XX
PI Sibbesen O, Sorensen JF;
XX
DR WPI; 2001-596834/67.
XX
DR P-FSDB; AAU07391.
XX
PT Novel variant xylanase polypeptide or its fragment useful for degrading
PT or modifying plant cell wall, comprises amino acid modifications such
PT that the polypeptide has altered sensitivity to xylanase inhibitor.
XX
PS Example 3; Page 43; 70pp; English.

XX
CC The invention relates to a variant xylanase polypeptide (I) or its
CC fragment having xylanase activity, comprising one or more amino acid
CC modifications such that (I) or its fragment has an altered sensitivity to
CC a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
CC its coding sequence (II) is useful for degrading or modifying plant cell
CC wall or for processing a plant material by contacting the plant cell wall
CC or plant material with (I) or (II). (I) is useful for modifying plant
CC materials, and in baking, processing cereals, starch production,
CC processing wood and enhancing the bleaching of wood pulp. (II) is useful
CC for altering the viscosity derived from the presence of hemicellulose or
CC arabinoxylan in a solution or system comprising plant cell wall material.
CC (I) is useful for preparing a foodstuff such as bread, pretzels,
CC tortillas, cakes, cookies, biscuits or crackers. The present sequence
CC represents the coding sequence of Bacillus subtilis xylanase as described
CC in the method of the invention

XX
SQ Sequence 645 BP; 192 A; 111 C; 163 G; 179 T; 0 U; 0 Other;

Query Match 43.9%; Score 79; DB 5; Length 645;
Best Local Similarity 79.0%; Pred. No. 3.4e-16;
Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 4 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 63

QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGGCGCCGACCATCACCATCACCATATCGAGGG 119
DB 64 TTGTTTTCGGACACCGCCTCTGCAGCTAGCAGACTACTGGCAAAATTCGACTGATGG 122

RESULT 11
ADC27538
ID ADC27538 standard; cDNA; 645 BP.
AC ADC27538;
XX
DT 18-DEC-2003 (first entry)
XX
DE Bacillus subtilis xylanase enzyme cDNA sequence.
KW xylanase; xylanase inhibitor; thermosensitivity; plant cell wall;
KW plant material; baking; processing cereal; starch production;
KW processing wood; wood pulp bleaching; animal feed; flour separation;
KW wetmilling; paper and pulp production; flour dough; hemicellulose;
KW arabinoxylan; food supplement; xylan; baking process; bread volume;
KW crumb structure; crumb appearance; shelf-life; gene; ss.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT CDS 4..645
FT /*tag= b
FT /*product= "Bacillus subtilis xylanase enzyme"

XX
FT sig_peptide 4..87
FT /*tag= a
FT mat_peptide 88..642
FT /*tag= c
FT /*label= Mature_Bacillus_subtilis_xylanase

XX
PN WO2003020923-A1.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-IB003797.
XX
PR 04-SEP-2001; 2001GB-00021387.
XX
PA (DANI-) DANISCO AS.
XX
PI Sibbesen O, Sorensen JF;
XX
DR WPI; 2003-332934/31.

CC The present sequence encodes a mutant endo-beta-1,4-xylanase. The
CC specification also describes an endo-beta-1,4-xylanase inhibitor, which
CC is obtained from wheat flour. The specification also describes a mutant
CC xylanase protein. The xylanase is useful for preparing a foodstuff,
CC preferably a bakery product or a substance (e.g. a dough) for making the
CC bakery product. Wild type xylanase or mutant xylanase is useful for
CC preparing a dough that is less sticky than a dough comprising a fungal
CC xylanase. The xylanase inhibitor is useful for screening high degree
CC resistance xylanases for dough preparation. The xylanase is also useful
CC for preparing a non-sticky dough. A combination of xylanase and the
CC inhibitor is useful for calibrating and/or determining the quantity of
CC inhibitor in a wheat flour sample

XX SQ Sequence 642 BP; 187 A; 115 C; 162 G; 178 T; 0 U; 0 Other;

Query Match 44.2%; Score 79.6; DB 3; Length 642;
Best Local Similarity 72.5%; Pred. No. 2.1e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGTTTAACTTTAAAGAGAAATCTTAGTGGGATTACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAACTTTAAAGAGAAATCTTAGTGGGATTACGGCAGCTTTCATGAGTATCAGC 60
QY 61 ATGTTTCTGCAACCGCTCTGCAGCTGCGCCGCAACATCACCATCACCATATCGAGGGA 120
DB 61 TTGTTTTCGGCAACCGCTCTGCAGCTAGCACAGACTACTGGCAAAATTGGACTGATGGG 120
QY 121 AGGACTCCGTAGGTCCAGCCA 142
DB 121 GCGGTACCGTAAACGCTGTCA 142

RESULT 8
AAA47156
ID AAA47156 standard; DNA; 642 BP.
AC AAA47156;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding a bacterial endo-beta-1,4-xylanase mutant XM2.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
KW dough; dough preparation; ss.
XX
OS Synthetic.
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT CDS 1..642
FT /*tag= a
FT /product= "xylanase mutant"
XX
PN WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX
PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
XX
XX (DANI-) DANISCO AS.
XX
XX Sibbesen O, Sorensen JF;
XX
XX WPI; 2000-465744/40.
XX P-PSDB; AAY93754.
XX
XX Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
PT
XX

PS Claim 3; Page 110; 112pp; English.

XX The present sequence encodes a mutant endo-beta-1,4-xylanase. The
CC specification also describes an endo-beta-1,4-xylanase inhibitor, which
CC is obtained from wheat flour. The specification also describes a mutant
CC xylanase protein. The xylanase is useful for preparing a foodstuff,
CC preferably a bakery product or a substance (e.g. a dough) for making the
CC bakery product. Wild type xylanase or mutant xylanase is useful for
CC preparing a dough that is less sticky than a dough comprising a fungal
CC xylanase. The xylanase inhibitor is useful for screening high degree
CC resistance xylanases for dough preparation. The xylanase is also useful
CC for preparing a non-sticky dough. A combination of xylanase and the
CC inhibitor is useful for calibrating and/or determining the quantity of
CC inhibitor in a wheat flour sample

XX SQ Sequence 642 BP; 189 A; 113 C; 161 G; 179 T; 0 U; 0 Other;

Query Match 44.2%; Score 79.6; DB 3; Length 642;
Best Local Similarity 72.5%; Pred. No. 2.1e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGTTTAACTTTAAAGAGAAATCTTAGTGGGATTACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAACTTTAAAGAGAAATCTTAGTGGGATTACGGCAGCTTTCATGAGTATCAGC 60
QY 61 ATGTTTCTGCAACCGCTCTGCAGCTGCGCCGCAACATCACCATCACCATATCGAGGGA 120
DB 61 TTGTTTTCGGCAACCGCTCTGCAGCTAGCACAGACTACTGGCAAAATTGGACTGATGGG 120
QY 121 AGGACTCCGTAGGTCCAGCCA 142
DB 121 GCGGTACCGTAAACGCTGTCA 142

RESULT 9
AAA47154
ID AAA47154 standard; DNA; 642 BP.
AC AAA47154;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding a bacterial endo-beta-1,4-xylanase protein.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
KW dough; dough preparation; ss.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT CDS 1..642
FT /*tag= a
FT /product= "xylanase"
XX
PN WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX
PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
XX
XX (DANI-) DANISCO AS.
XX
XX Sibbesen O, Sorensen JF;
XX
XX WPI; 2000-465744/40.
XX P-PSDB; AAY93752.
XX
XX Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
PT

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 21:23:54 ; Search time 937.383 Seconds
(without alignments)
8322.904 Million cell updates/sec

Title: US-10-009-792C-26

Perfect score: 180

Sequence: 1 atgtttaagtttaaaagaa.....tctgtccaagtgttagag 180

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rtd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	90.8	50.4	1620	1	BSU51675	U51675 Bacillus sp
2	89.2	49.6	641	6	A36647	A36647 Sequence 2
3	89.2	49.6	1413	6	A36646	A36646 Sequence 1
4	87.6	48.7	642	6	BD234184	BD234184 Proteins.
5	87.6	48.7	642	6	AX027170	AX027170 Sequence
6	79.6	44.2	642	6	BD234186	BD234186 Proteins.
7	79.6	44.2	642	6	BD234187	BD234187 Proteins.
8	79.6	44.2	642	6	BD234188	BD234188 Proteins.
9	79.6	44.2	642	6	AX027174	AX027174 Sequence
10	79.6	44.2	642	6	AX027176	AX027176 Sequence
11	79.6	44.2	642	6	AX027178	AX027178 Sequence
12	79.6	44.2	642	6	BD234185	BD234185 Proteins.
13	79.6	44.2	642	6	AX027172	AX027172 Sequence
14	79.6	44.2	642	6	AX244979	AX244979 Sequence
15	79.6	44.2	642	6	AX717003	AX717003 Sequence
16	79.6	44.2	642	6	AF490979	AF490979 Bacillus
17	79.6	44.2	642	6	AF441773	AF441773 Bacillus
18	79.6	44.2	642	6	BSXINS	BSXINS
19	79.6	44.2	642	6	BACKYNAB	BACKYNAB
20	79.6	44.2	642	6	BCXYLAG	BCXYLAG
21	79.6	44.2	642	6	BD247935	BD247935 Novel the
22	79.6	44.2	642	6	AX047508	AX047508 Sequence
23	79.6	44.2	642	6	AX608888	AX608888 Sequence
24	79.6	44.2	642	6	AF027868	AF027868 Bacillus
25	79.6	44.2	642	6	BSUB0011	BSUB0011
26	79.6	44.2	642	6	AF490980	AF490980 Bacillus
27	79.6	44.2	642	6	BSXYLAN	BSXYLAN
28	79.6	44.2	642	6	AX244980	AX244980 Sequence
29	79.6	44.2	642	6	AR000512	AR000512 Sequence
30	79.6	44.2	642	6	E11905	E11905 DNA encodin
31	79.6	44.2	642	6	BD017457	BD017457 Thermos
32	79.6	44.2	642	6	BD079063	BD079063 Bleacher
33	79.6	44.2	642	6	BD144645	BD144645 Thermos
34	79.6	44.2	642	6	AR202281	AR202281 Sequence
35	79.6	44.2	642	6	AR202282	AR202282 Sequence
36	79.6	44.2	642	6	AR223283	AR223283 Sequence
37	79.6	44.2	642	6	AR223284	AR223284 Sequence
38	79.6	44.2	642	6	E01423	E01423 DNA sequenc
39	79.6	44.2	642	6	I05086	I05086 Sequence 11
40	79.6	44.2	642	6	AR202204	AR202204 Sequence
41	79.6	44.2	642	6	AR223206	AR223206 Sequence
42	79.6	44.2	642	6	AR202223	AR202223 Sequence
43	79.6	44.2	642	6	AR202226	AR202226 Sequence
44	79.6	44.2	642	6	AR202229	AR202229 Sequence
45	79.6	44.2	642	6	AR202229	AR202229 Sequence

ALIGNMENTS

RESULT 1

BSU51675

LOCUS

DEFINITION

BSU51675

Bacillus sp. endo-1,4-beta-xylanhydrolase (xynA) gene, complete cds.

ACCESSION

U51675

VERSION

U51675.1

KEYWORDS

Bacillus sp.

SOURCE

Bacillus sp.

ORGANISM

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE

1 (bases 1 to 1620)

AUTHORS

Kim,S.C., Jeong,K.J. and Kim,M.S.

TITLE

Direct Submission

JOURNAL

BSU51675 1620 bp DNA linear BCT 31-JAN-1999
Bacillus sp. endo-1,4-beta-xylanhydrolase (xynA) gene, complete cds.

U51675 GI:4204770

Bacillus sp.

Bacillus sp.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 1620)

Kim,S.C., Jeong,K.J. and Kim,M.S.

Direct Submission

Submitted (18-MAR-1996) Sun Chang Kim, Biological Sciences, Korea

Advanced Institute of Science and Technology, 373-1, Kusong-dong
Yusong-ku, Taejeon 305-701, Korea

FEATURES

source
1. .1620
/organism="Bacillus sp."
/mol_type="genomic DNA"
/db_xref="taxon:1409"
360. .365
372. .1013
/genes="xynA"
372. .1013
/gene="xynA"
/function="xylan hydrolase"
/note="similar to B. subtilis xylanase, Swiss-Prot
Accession Number P18429"
/codon_start=1
/transl_table=11
/product="endo-1,4-beta-xylanhydrolase"
/protein_id="AAD10834.1"
/db_xref="GI:4204771"
/translation="MFKFKKPLVGLTAAPMSISMFSAATSAAGTDYWNWTDGGTV
NAVSGSGNYVNMNTGNFVVGKWTGSPRTINYNAGVWAPNGNGLIYGWTR
PLIEYVVDVSWGTYRPTGYKGVKSDGGTYDIYTTIRYNAPSIDGDNITFTQYMSVR
QSKRPTGSNAATITFSNHVNAWKSHGNLGSNWAYQVLATEGYKSGSSNVTVM"

ORIGIN

Query Match 50.4%; Score 90.8; DB 1; Length 1620;
Best Local Similarity 77.5%; Pred. No. 1.3e-19;
Matches 110; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 372 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 431
QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGCCGCCACCATCACCATATCGAGGGA 120
Db 432 ATGTTTCTGCAACCGCCTCTGCAGCTGCCGCCACCATCACCATATCGAGGGA 491
QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 492 GGCGGACAGTAACCGAGTCA 513

RESULT 2

A36647 641 bp DNA linear PAT 05-MAR-1997
LOCUS
DEFINITION Sequence 2 from Patent EP0585617.
ACCESSION A36647
VERSION A36647.1 GI:2293950
KEYWORDS
SOURCE
ORGANISM
Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE
1 (bases 1 to 641)
AUTHORS
Gotschalk, M.D., Schuster, E.D. and Sproesser, B.D.
TITLE
Bacterial Xylanase, method for its production and its application
in manufacturing bread
JOURNAL
Patent: EP 0585617-A 2 09-MAR-1994;
ROEHM GMBH (DE)
COMMENT
Other publication US 5306633 940426
Other publication FI 933519 940212
Other publication DE 4226528 940217.
Location/Qualifiers

FEATURES

source
1. .641
/organism="Bacillus subtilis"
/mol_type="unassigned DNA"
/strain="RH 1321"
/db_xref="taxon:1423"
1. .5641
/note="unassigned protein product"
/codon_start=1
/transl_table=11
/protein_id="CAA02246.1"

CDS

/db_xref="GI:2293951"

/db_xref="RENTREMBL:CAA02246"
/translation="MFKFKKPLVGLTAAPMSISMFSAATSAAGTDYWNWTDGGTV
NAVSGSGNYVNMNTGNFVVGKWTGSPRTINYNAGVWAPNGNGLIYGWTR
PLIEYVVDVSWGTYRPTGYKGVKSDGGTYDIYTTIRYNAPSIDGDNITFTQYMSVR
QSKRPTGSNAATITFSNHVNAWKSHGNLGSNWAYQVLATEGYKSGSSNVTVM"

ORIGIN

Query Match 49.6%; Score 89.2; DB 6; Length 641;
Best Local Similarity 76.8%; Pred. No. 3.7e-19;
Matches 109; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGCCGCCACCATCACCATATCGAGGGA 120
Db 61 ATGTTTCTGCAACCGCCTCTGCAGCTGCCGCCACCATCACCATATCGAGGGA 120
QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 121 GGCGGACAGTAACCGAGTCA 142

RESULT 3

A36646 1413 bp DNA linear PAT 05-MAR-1997
LOCUS
DEFINITION Sequence 1 from Patent EP0585617.
ACCESSION A36646
VERSION A36646.1 GI:2293949
KEYWORDS
SOURCE
ORGANISM
Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE
1 (bases 1 to 1413)
AUTHORS
Gotschalk, M.D., Schuster, E.D. and Sproesser, B.D.
TITLE
Bacterial Xylanase, method for its production and its application
in manufacturing bread
JOURNAL
Patent: EP 0585617-A 1 09-MAR-1994;
ROEHM GMBH (DE)
COMMENT
Other publication US 5306633 940426
Other publication FI 933519 940212
Other publication DE 4226528 940217.
Location/Qualifiers
FEATURES
source
1. .1413
/organism="Bacillus subtilis"
/mol_type="unassigned DNA"
/strain="RH 1321"
/db_xref="taxon:1423"

ORIGIN

Query Match 49.6%; Score 89.2; DB 6; Length 1413;
Best Local Similarity 76.8%; Pred. No. 4.3e-19;
Matches 109; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 506 ATGTTTAAAGTTTAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 565
QY 61 ATGTTTCTGCAACCGCCTCTGCAGCTGCCGCCACCATCACCATATCGAGGGA 120
Db 566 ATGTTTCTGCAACCGCCTCTGCAGCTGCCGCCACCATCACCATATCGAGGGA 120
QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 626 GGCGGACAGTAACCGAGTCA 647

RESULT 4

BD234184 642 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Proteins.


```

ACCESSION   BD234184
VERSION     BD234184.1  GI:33043954
KEYWORDS    JP 2002533121-A/1.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 642)
AUTHORS     Sibbesen,O. and Soerensen,J.F.
TITLE       Proteins
JOURNAL
COMMENT     Patent: JP 2002533121-A 1 08-OCT-2002;
            DANISCO AS
OS          Artificial Sequence
PN          JP 2002533121-A/1
PD          08-OCT-2002
PF          17-DEC-1999 JP 2000591181
PR          23-DEC-1998 GB 9828599.2,06-APR-1999 GB 9907805.7 PR
PI          OLE SIBBESSEN,JENS FRISBAEK SOERENSEN
PC          C12N15/09,A21D2/26,C07K14/415,C12N1/15,C12N1/19,C12N1/20 PC
PC          C12N1/21,C12N5/10,
PC          C12N9/42,C12P21/02,C12Q1/34,C12N15/00,C12N5/00 CC
Description of Artificial Sequence:wild-type xylanase FH Key
Location/Qualifiers
FT source 1..642
FT         /organism='Artificial Sequence'.

FEATURES
   source
       Location/Qualifiers
       1..642
       /organism="synthetic construct"
       /mol_type="genomic DNA"
       /db_xref="taxon:32630"

ORIGIN
Query Match 48.7%; Score 87.6; DB 6; Length 642;
Best Local Similarity 76.1%; Pred. No. 1.3e-18;
Matches 108; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60

QY 61 ATGTTTCTGCAACCGCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
DB 61 ATGTTTCTGCAACCGCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120

QY 121 AGGACTCCGTTAGTCCAGCCA 142
DB 121 GCGGGACAGTAACGCAGTCA 142

RESULT 6
LOCUS       BD234186
DEFINITION Proteins.
ACCESSION   BD234186
VERSION     BD234186.1  GI:33043956
KEYWORDS    JP 2002533121-A/3.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 642)
AUTHORS     Sibbesen,O. and Soerensen,J.F.
TITLE       Proteins
JOURNAL
COMMENT     Patent: JP 2002533121-A 3 08-OCT-2002;
            DANISCO AS
OS          Artificial Sequence
PN          JP 2002533121-A/3
PD          08-OCT-2002
PF          17-DEC-1999 JP 2000591181
PR          23-DEC-1998 GB 9828599.2,06-APR-1999 GB 9907805.7 PR
PI          OLE SIBBESSEN,JENS FRISBAEK SOERENSEN
PC          C12N15/09,A21D2/26,C07K14/415,C12N1/15,C12N1/19,C12N1/20 PC
PC          C12N1/21,C12N5/10,
PC          C12N9/42,C12P21/02,C12Q1/34,C12N15/00,C12N5/00 CC
Description of Artificial Sequence:mutant xylanase FH Key
Location/Qualifiers
FT source 1..642
FT         /organism='Artificial Sequence'.

FEATURES
   source
       Location/Qualifiers
       1..642
       /organism="synthetic construct"
       /mol_type="genomic DNA"
       /db_xref="taxon:32630"

ORIGIN
Query Match 44.2%; Score 79.6; DB 6; Length 642;
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60

QY 61 ATGTTTCTGCAACCGCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
DB 61 TTGTTTTCGGCAACCGCTCTGCAGCTAGCAGACTACTGGCAAAATTGGACTGATGGG 120

QY 121 AGGACTCCGTTAGTCCAGCCA 142
DB 121 GCGGGTACCGTAAACGCAGTCA 142

RESULT 7
LOCUS       BD234187
DEFINITION Proteins.
Query Match 48.7%; Score 87.6; DB 6; Length 642;
Best Local Similarity 76.1%; Pred. No. 1.3e-18;
Matches 108; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGGATTAAACGGCAGCTTTCATGAGTATCAGC 60

QY 61 ATGTTTCTGCAACCGCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
DB 61 ATGTTTCTGCAACCGCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120

QY 121 AGGACTCCGTTAGTCCAGCCA 142
DB 121 GCGGGTACCGTAAACGCAGTCA 142

RESULT 7
LOCUS       BD234187
DEFINITION Proteins.

```

```

ACCESSION      BD234187
VERSION        BD234187.1 GI:33043957
KEYWORDS       JP 2002533121-A/4.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 642)
AUTHORS        Sibbesen,O. and Soerensen,J.F.
TITLE          Proteins
JOURNAL        DANISCO AS
COMMENT        Patent: JP 2002533121-A 4 08-OCT-2002;
              OS Artificial Sequence
              PN JP 2002533121-A/4
              PD 08-OCT-2002
              PF 17-DEC-1999 JP 2000591181
              PR 23-DEC-1998 GB 9828599.2,06-APR-1999 GB 9907805.7 PR
              PI OLE STIBBESEN,JENS FRISBAEK SOERENSEN
              PC C12N15/09,A21D2/26,C07K14/415,C12N1/15,C12N1/19,C12N1/20 PC
              ,C12N1/21,C12N5/10,
              PC C12N9/42,C12P21/02,C12Q1/34,C12N15/00,C12N5/00 CC
              Description of Artificial Sequence:mutant xylanase FH
              Location/Qualifiers
              FT source 1..642
              /organism='Artificial Sequence'.

FEATURES
  source      Location/Qualifiers
              1..642
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Query Match 44.2%; Score 79.6; DB 6; Length 642;
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60
Db 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60
QY 61 ATGTTTCTGCAACCGCCTCTGCAGTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
Db 61 TTGTTTTCGGCAACCGCCTCTGCAGTAGCAGACAGACTACTGGCAAAATTGGACTGATGG 120
QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 121 GCGGTACCGTAAACGCTGTCA 142

RESULT 9
AX027174
LOCUS         AX027174 642 bp DNA linear PAT 16-SEP-2000
DEFINITION   Sequence 8 from Patent WO0039289.
ACCESSION    AX027174
VERSION      AX027174.1 GI:10188159
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      Soerensen,J.F. and Sibbesen,O.
TITLE        Proteins
JOURNAL      SOERENSEN JENS FRISBAEK (DK) ; DANISCO (DK) ; STIBBESEN OLE (DK)
FEATURES
  source      Location/Qualifiers
              1..642
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="mutant xylanase"

ORIGIN
Query Match 44.2%; Score 79.6; DB 6; Length 642;
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60
Db 1 ATGTTTAAGTTTAAAGAAGAAATCTTAGTGGGATTAAACGGCAGCTTTCATGATATCAGC 60
QY 61 ATGTTTCTGCAACCGCCTCTGCAGTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
Db 61 TTGTTTTCGGCAACCGCCTCTGCAGTAGCAGACAGACTACTGGCAAAATTGGACTGATGG 120
QY 121 AGGACTCCGTTAGTCCAGCCA 142
Db 121 GCGGTACCGTAAACGCTGTCA 142

RESULT 10
AX027176
LOCUS         AX027176 642 bp DNA linear PAT 16-SEP-2000
DEFINITION   Sequence 10 from Patent WO0039289.

```

ACCESSION AX027176
VERSION AX027176.1 GI:10188160
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Soerensen, J.F. and Sibbesen, O.
TITLE Proteins
JOURNAL Patent: WO 0039289-A 10 06-JUL-2000;
SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESSEN OLE (DK)
FEATURES
source
1..642
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="mutant xylanase"
ORIGIN
Query Match 44.2%; Score 79.6; DB 6; Length 642;
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
QY 61 ATGTTTTCGCAACCGCTCTCAGCTGCGCCGACCATCACCATCACCATCAGGGA 120
DB 61 TTGTTTTCGCAACCGCTCTCAGCTGCGCCGACCATCACCATCACCATCAGGGA 120
QY 121 AGGACTCCGTTAGGTCCAGCCA 142
DB 121 GCGGTACCGTAAACGCTGTCA 142
RESULT 11
AX027178
LOCUS 642 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 12 from Patent WO0039289.
ACCESSION AX027178
VERSION AX027178.1 GI:10188161
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Soerensen, J.F. and Sibbesen, O.
TITLE Proteins
JOURNAL Patent: WO 0039289-A 12 06-JUL-2000;
SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESSEN OLE (DK)
FEATURES
source
1..642
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="mutant xylanase"
ORIGIN
Query Match 44.2%; Score 79.6; DB 6; Length 642;
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
QY 61 ATGTTTTCGCAACCGCTCTCAGCTGCGCCGACCATCACCATCACCATCAGGGA 120
DB 61 TTGTTTTCGCAACCGCTCTCAGCTGCGCCGACCATCACCATCACCATCAGGGA 120
QY 121 AGGACTCCGTTAGGTCCAGCCA 142

Db 121 GCGGTACCGTAAACGCTGTCA 142
RESULT 12
BD234185
LOCUS 642 bp DNA linear PAT 17-JUL-2003
DEFINITION Proteins
ACCESSION BD234185
VERSION BD234185.1 GI:33043955
KEYWORDS JP 2002533121-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 642)
AUTHORS Sibbesen, O. and Soerensen, J.F.
TITLE Proteins
JOURNAL Patent: JP 2002533121-A 2 08-OCT-2002;
DANISCO AS
COMMENT OS Artificial Sequence
PN JP 2002533121-A/2
PD 08-OCT-2002
PF 17-DEC-1999 JP 2000591181
PR 23-DEC-1998 GB 9828599.2, 06-APR-1999 GB 9907805.7 PR
PI 15-APR-1999 GB 9908645.6
PC C12N15/09, A21D2/26, C07K14/415, C12N1/15, C12N1/19, C12N1/20 PC
C12N1/21, C12N5/10.
PC C12N9/42, C12P21/02, C12O1/34, C12N15/00, C12N5/00 CC
Description of Artificial Sequence: wild-type xylanase FH Key
FEATURES
source
1..642
Location/Qualifiers
FT source
1..642
/organism="Artificial Sequence".
ORIGIN
Query Match 43.9%; Score 79; DB 6; Length 642;
Best Local Similarity 79.0%; Pred. No. 1.2e-15;
Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
DB 1 ATGTTTAAGTTTAAAGAAATTCCTAGTGGATTAAACGGCAGCTTTCATGAGTATCAGC 60
QY 61 ATGTTTTCGCAACCGCTCTCAGCTGCGCCGACCATCACCATCACCATCAGGGA 119
DB 61 TTGTTTTCGCAACCGCTCTCAGCTGCGCCGACCATCACCATCACCATCAGGGA 119
RESULT 13
AX027172
LOCUS 642 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 6 from Patent WO0039289.
ACCESSION AX027172
VERSION AX027172.1 GI:10188158
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Soerensen, J.F. and Sibbesen, O.
TITLE Proteins
JOURNAL Patent: WO 0039289-A 6 06-JUL-2000;
SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESSEN OLE (DK)
FEATURES
source
1..642
Location/Qualifiers
FT source
1..642
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="wild-type xylanase"

```

Best Local Similarity 79.0%; Pred.No. 1.2e-15;
Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTTAAACGGCAGCTTTTCATGAGTATCAGC 60
   |||||
Db 4 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTTATCGGCAGCTTTAAATGAGTATTAGC 63
   |||||

Qy 61 ATGTTTTTCTGCAACCGGCTCTGAGCTGGCCCGCACCATCACCATATTCGAGGG 119
   |||||

Db 64 TTGTTTTCGCAACCGGCTCTGAGCTAGCACAGACTACTGGCAAAATTGGCACTGATGG 122
   |||||

Search completed: October 9, 2004, 03:08:35
Job time : 941.383 secs

```

```

ORIGIN
Query Match          43.9%;   Score 79;   DB 6;   Length 642;
Best Local Similarity 79.0%;   Pred. No. 1.2e-15;
Matches 94;   Conservative 0;   Mismatches 25;   Indels 0;   Gaps 0;

QY      1  ATGTTTAAAGTTTAAAAAGAAATTCCTTAGTCGGATTAAACGCGAGCTTTCATGAGTATCAGC 60
Db      1  ATGTTTAAAGTTTAAAAAGAAATTCCTTAGTTGGATTATCGCGAGCTTTCATGAGTATTAGC 60

QY      61  ATGTTTTCTGCAACCGGCTCTGCGAGCTGGCCCGCACCATCACCATATCGAGGG 119
Db      61  TTGTTTTTCGGCAACCGGCTCTGCGAGCTAGCACAGACTACTGGCAAAATTTGGACTCATGG 119

```

RESULT	14
LOCUS	AX244979
DEFINITION	Sequence 10 from Patent WO0166711.
ACCESSION	AX244979
VERSION	AX244979.1 GI:15859704
KEYWORDS	.
SOURCE	Bacillus subtilis
ORGANISM	Bacillus subtilis Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus..
REFERENCE	1 Sibbesen,O. and Sorensen,J.F. Xylanase variants having altered sensitivity to xylanase inhibitors Patent: WO 0166711-A 10-SEP-2001; DANISCO A/S (DK)
AUTHORS	
TITLE	
JOURNAL	

ORIGIN	Query Match	43.9%	Score 79	DB 6	Length 645
	Best Local Similarity	79.0%	Pred. No. 1.2e-15		
	Matches 94	Conservative 0	Mismatches 25	Indels 0	Gaps 0
QY	1	ATGTTTAAAGTTTAAAAAGAAATCTTTAGTCGGATTAAACGGCAGCTTTTCATGAGTATACGC	60		
		TTGTTTTCGGCAACCGGCTCTTCGAGCTAGCACAGACTACTGGCAAAATTTGGACTGATGG	122		
Db	4	ATGTTTAAAGTTTAAAAAGAAATCTTTAGTTGGATTATCGCAGCTTTAATGAGTATTAGC	63		
QY	61	ATGTTTTTCTGCAACCGGCTCTTCGAGCTGGCGCGCACATCACCATCATTCAGGG	119		

```

RESULT 15
AX717003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
    source
        linear
        DNA
        645 bp
        Sequence 9 from Patent WO03020923.
        AX717003
        AX717003.1 GI:29890250
        Bacillus subtilis
        Bacillus subtilis
        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
        Sibbesen,O. and Soerensen,J.F.
        Xylanase variants
        Patent: WO 03020923-A 9 13-MAR-2003;
        DANISCO A/S (DK)
        Location/Qualifiers
            1..645
            /organism="Bacillus subtilis"
            /mol_type="unassigned DNA"
            /db_xref="taxon:1423"

```

ORIGIN	Query Match	Score 79;	DB 6;	Length 645;
/w_xref=cax01.1423	43.9%			

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 00:53:40 ; Search time 3228.76 Seconds
(without alignments)
4837.123 Million cell updates/sec

Title: US-10-009-792c-18_COPY_88_610

Perfect score: 523

Sequence: 1 accccctgggcccctgcag.....acgcacactggccagccct 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gsl:*
- 29: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523	100.0	906	14	CA487627
2	523	100.0	1080	12	EM553432
3	523	100.0	1123	12	EM554035
4	522	99.8	983	12	EM557421

5	521.4	99.7	897	14	CD013924
6	521.4	99.7	1096	12	BM923410
7	521.4	99.7	1141	12	BM906188
8	506.2	96.8	1445	12	BM906367
9	504	96.4	624	29	AY414900
10	499.4	95.5	993	12	BM915836
11	497.6	95.1	608	29	AY414901
12	489.4	93.6	990	12	BM423896
13	485.6	92.8	986	14	CA487516
14	483	92.4	1012	12	BM556479
15	426	81.5	554	14	CB126975
16	423.4	81.0	817	12	EM003358
17	419.4	80.2	874	14	CA489884
18	375.6	71.8	570	12	BI961242
19	355.6	68.0	548	12	BI960812
20	332.6	63.6	973	12	BI411128
21	313.8	60.0	598	12	BG548320
22	313.8	60.0	789	14	CD013925
23	313.6	60.0	642	29	AY414902
24	310	59.3	829	12	BM009247
25	309.4	59.2	622	14	CD013926
26	307.8	58.9	952	14	CA487806
27	300.6	57.5	507	10	B3485194
28	284	54.3	346	14	CB705562
29	275.4	52.7	579	14	CB127794
30	263.4	50.4	1375	12	BM554037
31	245.8	47.0	802	14	CA489740
32	245.8	47.0	948	12	BI822673
33	213	40.7	368	12	BI961002
34	200.4	38.3	466	14	CB714821
35	189	36.1	314	14	CB136760
36	180.4	34.5	509	12	BM256261
37	137.4	26.3	392	13	BY022511
38	135.8	26.0	327	10	BF848766
39	110.8	21.2	385	13	BY024867
40	99.6	19.0	380	13	BY027389
41	99	18.9	1123	12	BM807686
42	96.4	18.4	380	13	BY026163
43	96.2	18.4	582	29	CB128466
44	91.8	17.6	382	13	BY026876
45	90.2	17.2	370	13	BY023671

ALIGNMENTS

RESULT 1
CA487627
LOCUS CA487627 906 bp mRNA linear EST 14-NOV-2002
DEFINITION AGENCOURT_10808790 MAPcL Homo sapiens cDNA clone IMAGE:6719127 5', mRNA sequence.
ACCESSION CA487627 GI:24947489
VERSION CA487627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 906)
NHL-MGC <http://mgc.nhl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAMA4276 row: i column: 15
High quality sequence stop: 712.

CD013924 90138839
BM923410 AGENCOURT
BM906188 AGENCOURT
BM906367 AGENCOURT
AY414900 Homo sapi
BM915836 AGENCOURT
AY414901 Pan trogl
BM423896 AGENCOURT
CA487516 AGENCOURT
BM556479 AGENCOURT
CB126975 K-EST0176
EM003358 603629823
CA489884 AGENCOURT
BI961242 MONO1_7 G
BI960812 MONO1_1 B
BI411128 602962472
BG548320 602575289
CD013925 90138939
AY414902 Mus muscu
BM009247 603629863
CD013926 90138855
CA487806 AGENCOURT
BE485194 172130 BA
CB705562 AMGNNUC:T
CB127794 K-EST0177
BM554037 AGENCOURT
CA489740 AGENCOURT
BI822673 603036006
BI961002 MONO1_3 H
CB714821 AMGNNUC:H
CB136760 K-EST0189
BM256261 518592 MA
BY022511 BY022511
BF848766 QVO-ENO10
BY024867 BY024867
BY027389 BY027389
BM807686 AGENCOURT
BY026163 BY026163
CB128466 tigr-gas-
BY026876 BY026876
BY023671 BY023671

```

FEATURES
  source
    Location/Qualifiers
      1..906
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:6719127"
        /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
        hERT-HME1, LNCap"
        /lab_host="MDH10B"
        /clone_lib="MAPcL"
        /notes="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
        Subtracted with brain, liver, lung, kidney and muscle.
        Directionally cloned. Priming method: oligo-dT. Average
        insert size: 1800 bp. Library amplification: 26,000 fold.
        Kristi A. Eglant, James J. Vincent, Robert Strausberg,
        Bungkook Lee & Ira Pastan: Discovery of new breast
        cancer genes encoding membrane and secreted proteins.
        Manuscript submitted."
      ORIGIN
        Query Match 100.0%; Score 523; DB 14; Length 906;
        Best Local Similarity 100.0%; Pred. No. 7.3e-97;
        Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 1 ACCCCCTGGCCCTCCAGCTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 60
        Db 80 ACCCCCTGGCCCTCCAGCTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 139
        QY 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAACTGTGTGCCACCTACAAG 120
        Db 140 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAACTGTGTGCCACCTACAAG 199
        QY 121 CTGTGCCACCCGAGAGCTGTGTCTGCTCGGACACTCTCTGGGATCCCTGGGCTCCC 180
        Db 200 CTGTGCCACCCGAGAGCTGTGTCTGCTCGGACACTCTCTGGGATCCCTGGGCTCCC 259
        QY 181 CTGAGCAGCTGCCCCAGCCCTTGACGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
        Db 260 CTGAGCAGCTGCCCCAGCCCTTGACGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 319
        QY 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTGGAGGGATCTCCCGAGTTGGGT 300
        Db 320 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTGGAGGGATCTCCCGAGTTGGGT 379
        QY 301 CCCACCTTGACACACTGACGTGGACGTGCGCGACTTTGCCACCACTCTGGCAGCAG 360
        Db 380 CCCACCTTGACACACTGACGTGGACGTGCGCGACTTTGCCACCACTCTGGCAGCAG 439
        QY 361 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCCACTCCAGGGTGCCATGCCGCGCTTC 420
        Db 440 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCCACTCCAGGGTGCCATGCCGCGCTTC 499
        QY 421 GCCTCTGCTTTCCAGCGCGGCGAGAGGGGTCCTAGTTGCTCCATCTGCAGAGCTTC 480
        Db 500 GCCTCTGCTTTCCAGCGCGGCGAGAGGGGTCCTAGTTGCTCCATCTGCAGAGCTTC 559
        QY 481 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCCAGCCCT 523
        Db 560 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCCAGCCCT 602

RESULT 2
BM553432 1080 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6572502 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5467250
DEFINITION 5', mRNA sequence.
ACCESSION BM553432
VERSION BM553432.1 GI:18792155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

1 (bases 1 to 1080)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: csapbs@mail.nih.gov
 Tissue Procurement: DCID/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1968 row: p column: 03
 High quality sequence stop: 746.

FEATURES

Location/Qualifiers
 1..1080
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5467250"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 41"
 /notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 523; DB 12; Length 1080;
 Best Local Similarity 100.0%; Pred. No. 7.9e-97;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 60
 Db 145 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 204
 QY 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAACTGTGTGCCACCTACAAG 120
 Db 205 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAACTGTGTGCCACCTACAAG 264
 QY 121 CTGTGCCACCCGAGAGCTGTGTCTGCTCGGACACTCTCTGGGATCCCTGGGCTCCC 180
 Db 265 CTGTGCCACCCGAGAGCTGTGTCTGCTCGGACACTCTCTGGGATCCCTGGGCTCCC 324
 QY 181 CTGAGCAGCTGCCCCAGCCCTTGACGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
 Db 325 CTGAGCAGCTGCCCCAGCCCTTGACGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 384
 QY 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTGGAGGGATCTCCCGAGTTGGGT 300
 Db 385 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTGGAGGGATCTCCCGAGTTGGGT 444
 QY 301 CCCACCTTGACACACTGACGTGGACGTGCGCGACTTTGCCACCACTCTGCGAGCAG 360
 Db 445 CCCACCTTGACACACTGACGTGGACGTGCGCGACTTTGCCACCACTCTGCGAGCAG 504
 QY 361 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCCACTCCAGGGTGCCATGCCGCGCTTC 420
 Db 505 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCCACTCCAGGGTGCCATGCCGCGCTTC 564
 QY 421 GCCTCTGCTTTCCAGCGCGGCGAGAGGGGTCTAGTTGCTCCATCTGCAGAGCTTC 480
 Db 565 GCCTCTGCTTTCCAGCGCGGCGAGAGGGGTCTAGTTGCTCCATCTGCAGAGCTTC 624
 QY 481 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCCAGCCCT 523
 Db 625 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCCAGCCCT 667

RESULT 3
BM554035 1123 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6580951 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469210
DEFINITION 5', mRNA sequence.
ACCESSION BM554035
VERSION BM554035.1 GI:18793290
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1123)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1974 row: a column: 19
High quality sequence stop: 753.

FEATURES
source
1..1123
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5469210"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 523; DB 12; Length 1123;
Best Local Similarity 100.0%; Pred. No. 8e-97;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTCTCAAGTGTAGAGCAA 60
DB 146 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTCTCAAGTGTAGAGCAA 205
QY 61 GTGAGGAGATCCAGGGCGATGGCGAGCGTCCAGGAGAGCTGTGTGCCACCTACAAG 120
DB 206 GTGAGGAGATCCAGGGCGATGGCGAGCGTCCAGGAGAGCTGTGTGCCACCTACAAG 265
QY 121 CTGTGCCACCCGAGAGCTGTGTGTCTGTGGACACTCTCTGGGATCCCTGGGCTCCC 180
DB 266 CTGTGCCACCCGAGAGCTGTGTGTCTGTGGACACTCTCTGGGATCCCTGGGCTCCC 325
QY 181 CTGAGCAGTGGCCCGAGCGCCCTGCAGCTGGCAGGCTGTGTGGACCACTCATAGC 240
DB 326 CTGAGCAGTGGCCCGAGCGCCCTGCAGCTGGCAGGCTGTGTGGACCACTCATAGC 385
QY 241 GGCCTTTTCTTACCAGGGGCTCTGTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 300
DB 386 GGCCTTTTCTTACCAGGGGCTCTGTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 445
QY 301 CCCACCTTGGACACTGTCAGCTGGACGTGCGCGACTTGGCCACCACCATCTGGCAGCAG 360

DB 446 CCCACCTTGGACACACTGCAGCTGGAGCTGGCGAGCTTTGCCACCACCATCTGGCAGCAG 505
QY 361 ATGGAAGAACTGGGAATGCCCTGCTGAGCCACCCAGGCTGCCATGCGGCGCTTC 420
DB 506 ATGGAAGAACTGGGAATGCCCTGCTGAGCCACCCAGGCTGCCATGCGGCGCTTC 565
QY 421 GCCTCTGCTTTCCAGCGCGGCGAGAGGGTCTTAGTTGCTCTCCATCTGCAGAGCTTC 480
DB 566 GCCTCTGCTTTCCAGCGCGGCGAGAGGGTCTTAGTTGCTCTCCATCTGCAGAGCTTC 625
QY 481 CTGAGAGTCTGTACCGCGTCTTACGCCACCTTGGCCAGCCCT 523
DB 626 CTGAGAGTCTGTACCGCGTCTTACGCCACCTTGGCCAGCCCT 668

RESULT 4
BM557421 983 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_5578800 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5466747
DEFINITION 5', mRNA sequence.
ACCESSION BM557421
VERSION BM557421.1 GI:18799394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 983)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1967 row: k column: 04
High quality sequence stop: 593.

FEATURES
source
1..983
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5466747"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 99.0%; Score 522; DB 12; Length 983;
Best Local Similarity 99.0%; Pred. No. 1.2e-96;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTCTCAAGTGTAGAGCAA 60
DB 145 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTCTCAAGTGTAGAGCAA 204
QY 61 GTGAGGAGATCCAGGGCGATGGCGAGCGTCCAGGAGAGCTGTGTGCCACCTACAAG 120
DB 205 GTGAGGAGATCCAGGGCGATGGCGAGCGTCCAGGAGAGCTGTGTGCCACCTACAAG 264

QY 121 CTGTGCACCCCGAGAGCTGGTCTCGACACTCTCTGGGCATCCCTTGGGCTCCC 180
 DB 265 CTGTGCCACCCCGAGAGCTGGTCTCGACACTCTCTGGGCATCCCTTGGGCTCCC 324
 QY 181 CTGAGAGCTGCCCCAGCAGCCCTGCGAGCTGGAGGCTGCTTGAGCCAACTCCATAGC 240
 DB 325 CTGAGAGCTGCCCCAGCAGCCCTGCGAGCTGGAGGCTGCTTGAGCCAACTCCATAGC 384
 QY 241 GGCCTTTTCTCTACACAGGCGCTCTGCGAGCCCTGGAAGGATCTCCGCCAGTTGGGT 300
 DB 385 GGCCTTTTCTCTACACAGGCGCTCTGCGAGCCCTGGAAGGATCTCCGCCAGTTGGGT 444
 QY 301 CCCACCTTGACACACTGAGCTGGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 360
 DB 445 CCCACCTTGACACACTGAGCTGGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 504
 QY 361 ATGGAGAACTGGGAATGGCCCTGCTGCGAGCCCTGCGAGCCCTGCGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 420
 DB 505 ATGGAGAACTGGGAATGGCCCTGCTGCGAGCCCTGCGAGCCCTGCGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 564
 QY 421 GCCTCTGCTTTCCAGCGCCGCGGAGGAGGCTCTAGTTGCCCTCCATCTGCAGAGCTTC 480
 DB 565 GCCTCTGCTTTCCAGCGCCGCGGAGGAGGCTCTAGTTGCCCTCCATCTGCAGAGCTTC 624
 QY 481 CTGGAGGTGCTGACCGGCTTCTACGCGACCTTGCCAGCCCT 523
 DB 625 CTGGAGGTGCTGACCGGCTTCTACGCGACCTTGCCAGCCCT 667

RESULT 5

CD013924 897 bp mRNA linear EST 21-OCT-2003
 LOCUS 90139839 Single gene library Homo sapiens cDNA, mRNA sequence.
 CD013924
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 897)
 Au-Young, J. and Stuve, L.L.
 Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
 Au-Young, J. and Stuve, L.L.
 PCR isolation and cloning of novel splice variant mRNAs from known
 drug target genes
 Unpublished (2003)
 Contact: Jin, P.
 Incyte Corporation
 3160 Porter Drive, Palo Alto, CA 94304, USA
 Tel: 650 621 8639
 Fax: 650 621 8965
 Email: pj@incyte.com

Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="Single gene library"
 /note="Vector: pDrive Cloning Vector; RT-PCR was performed
 using gene-specific primers flanking the open-reading
 frame. PCR products were subcloned into pDrive Cloning
 Vector and sequenced completely using M13 forward and
 reverse primers. Sequencing gaps were closed by
 re-sequencing using primers flanking the gapped areas."

FEATURES
 source
 Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="Single gene library"
 /note="Vector: pDrive Cloning Vector; RT-PCR was performed
 using gene-specific primers flanking the open-reading
 frame. PCR products were subcloned into pDrive Cloning
 Vector and sequenced completely using M13 forward and
 reverse primers. Sequencing gaps were closed by
 re-sequencing using primers flanking the gapped areas."

ORIGIN
 Query Match 99.7%; Score 521.4; DB 14; Length 897;
 Best Local Similarity 99.8%; Pred. No. 1.5e-96;
 Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTCTTAGAGCAA 60
 |||||

Db 275 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGTTCCTGTCAAGTCTTAGAGCAA 334
 QY 61 GTGAGGAAGATCCAGGCGGATGGCGAGCGCTCCAGGAGAAGCTGTGTGCCACTCAAG 120
 DB 335 GTGAGGAAGATCCAGGCGGATGGCGAGCGCTCCAGGAGAAGCTGTGTGCCACTCAAG 394
 QY 121 CTGTGCCACCCCGAGAGCTGGTCTGCTCGGACACTCTCTGGGCATCCCTTGGGCTCCC 180
 DB 395 CTGTGCCACCCCGAGGAGCTGGTCTGCTCGGACACTCTCTGGGCATCCCTTGGGCTCCC 454
 QY 181 CTGAGGAGCTGCCCCAGCAGGCGCTGCGAGCTGGAGGCTGCTTGAGCCAACTCCATAGC 240
 DB 455 CTGAGGAGCTGCCCCAGCAGGCGCTGCGAGCTGGAGGCTGCTTGAGCCAACTCCATAGC 514
 QY 241 GGCCTTTTCTCTACCAAGGGGCTCTGCGAGCGCTTGAAGGGATCTCCGCCAGTTGGGT 300
 DB 515 GGCCTTTTCTCTACCAAGGGGCTCTGCGAGCGCTTGAAGGGATCTCCGCCAGTTGGGT 574
 QY 301 CCCACCTTGACACACTGAGCTGGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 360
 DB 575 CCCACCTTGACACACTGAGCTGGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 634
 QY 361 ATGGAGAACTGGGAATGGCCCTGCTGCGAGCCCTGCGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 420
 DB 635 ATGGAGAACTGGGAATGGCCCTGCTGCGAGCCCTGCGAGCTGGCGACTTTGCCACCACTCTGGCAGCAG 694
 QY 421 GCCTCTGCTTTCCAGCGCCGCGGAGGAGGCTCTAGTTGCCCTCCATCTGCAGAGCTTC 480
 DB 695 GCCTCTGCTTTCCAGCGCCGCGGAGGAGGCTCTAGTTGCCCTCCATCTGCAGAGCTTC 754
 QY 481 CTGGAGGTGCTGACCGGCTTCTACGCGACCTTGCCAGCCCT 523
 DB 755 CTGGAGGTGCTGACCGGCTTCTACGCGACCTTGCCAGCCCT 797

RESULT 6

BM923410 1096 bp mRNA linear EST 12-MAR-2002
 LOCUS 6625827 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5759022
 DEFINITION
 5' mRNA sequence.
 ACCSSSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1096)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@nsl.nih.gov

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12803 Row: m Column: 07
 High quality sequence stop: 646.
 Location/Qualifiers
 1..1096
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5759022"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo

FEATURES
 source
 Location/Qualifiers
 1..1096
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5759022"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo

FEATURES

source
 Location/Qualifiers
 1..1096
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5759022"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 99.7%; Score 521.4; DB 12; Length 1096;
Best Local Similarity 99.8%; Pred. No. 1.7e-96;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCGAGTCCCTGCCCGAGAGTCTCTGCTCAAGTGTAGAGCAA 60
DB 129 ACCCCCTGGCCCTGCGAGTCCCTGCCCGAGAGTCTCTGCTCAAGTGTAGAGCAA 188
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGTGTGTGCGACCTACAAG 120
DB 189 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGTGTGTGCGACCTACAAG 248
QY 121 CTGTGCCACCCGAGGAGCTGTGCTGCTCGGACACTCTGCGCATCCCTGGGCTCCC 180
DB 249 CTGTGCCACCCGAGGAGCTGTGCTGCTCGGACACTCTGCGCATCCCTGGGCTCCC 308
QY 181 CTGAGCAGCTGCCCCAGCCAGGCGCTGCGAGTGGCAGGCTCTTGAGCCAACTCCATAGC 240
DB 309 CTGAGCAGCTGCCCCAGCCAGGCGCTGCGAGTGGCAGGCTCTTGAGCCAACTCCATAGC 368
QY 241 GGCCTTTTCTTACAGGGGCTGCTGCGAGGCGCTGCGAGGAGTCTGCGCGAGTTGGGT 300
DB 369 GGCCTTTTCTTACAGGGGCTGCTGCGAGGCGCTGCGAGGAGTCTGCGCGAGTTGGGT 428
QY 301 CCCACCTTGGACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 360
DB 429 CCCACCTTGGACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 488
QY 361 ATGGAAGAAGTGGGAATGGCCCTGCTGCGAGGCGCTGCGAGGAGTCTGCGCGAGTTGGGT 420
DB 489 ATGGAAGAAGTGGGAATGGCCCTGCTGCGAGGCGCTGCGAGGAGTCTGCGCGAGTTGGGT 548
QY 421 GCCTCTGCTTTCCAGCGCGGGCAGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 549 GCCTCTGCTTTCCAGCGCGGGCAGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY 481 CTGAGAGTGTGCTACCGCGTCTTACGCCACCTTGGCCAGCCCT 523
DB 609 CTGAGAGTGTGCTACCGCGTCTTACGCCACCTTGGCCAGCCCT 651

RESULT 7

BM906188
LOCUS
DEFINITION
AGENCOURT_6621301 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590090
5', mRNA sequence.

ACCESSION
BM906188
VERSION
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1141)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Place: LLNL2363 row: n column: 11
High quality sequence start: 10
High quality sequence stop: 599.
Location/Qualifiers
1. .1141

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590090"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT2;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN

Query Match 99.7%; Score 521.4; DB 12; Length 1141;
Best Local Similarity 99.8%; Pred. No. 1.7e-96;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCGAGTCCCTGCCCGAGAGTCTCTGCTCAAGTGTAGAGCAA 60
DB 127 ACCCCCTGGCCCTGCGAGTCCCTGCCCGAGAGTCTCTGCTCAAGTGTAGAGCAA 186
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGTGTGTGCGACCTACAAG 120
DB 187 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGTGTGTGCGACCTACAAG 246
QY 121 CTGTGCCACCCGAGGAGCTGTGCTGCTCGGACACTCTCTGCGCATCCCTGGGCTCCC 180
DB 247 CTGTGCCACCCGAGGAGCTGTGCTGCTCGGACACTCTCTGCGCATCCCTGGGCTCCC 306
QY 181 CTGAGCAGTGTGCCACAGCGCTTGCAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
DB 307 CTGAGCAGTGTGCCACAGCGCTTGCAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 366
QY 241 GGCCTTTTCTTACAGGGGCTCTGCGAGGCGCTGGAAGGATCTCTCCCGAGTTGGGT 300
DB 367 GGCCTTTTCTTACAGGGGCTCTCTGCGAGGCGCTGGAAGGATCTCTCCCGAGTTGGGT 426
QY 301 CCCACCTTGGACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 360
DB 427 CCCACCTTGGACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 486
QY 361 ATGGAAGAAGTGGGAATGGCCCTGCTGCGAGGCGCTGCGAGGAGTCTGCGCGAGTTGGGT 420
DB 487 ATGGAAGAAGTGGGAATGGCCCTGCTGCGAGGCGCTGCGAGGAGTCTGCGCGAGTTGGGT 546
QY 421 GCCTCTGCTTTCCAGCGCGGGCAGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 547 GCCTCTGCTTTCCAGCGCGGGCAGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 481 CTGAGAGTGTGCTACCGCGTCTTACGCCACCTTGGCCAGCCCT 523
DB 607 CTGAGAGTGTGCTACCGCGTCTTACGCCACCTTGGCCAGCCCT 649

RESULT 8

BM906367
LOCUS
DEFINITION
AGENCOURT_6620268 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590315
5', mRNA sequence.

ACCESSION
BM906367
VERSION
BM906367.1 GI:19356746


```

Db      391  GAGTTGGTCCCACTTGGACACACTGAGCTGAGCTGCGGACTTGGCCACCAATC 450
Qy      352  TGGCAGCAGATGGAAGAACTGGGAATGCCCCCTGCTGAGCCACCCAGGGTGCATG 411
Db      451  TGGCAGCAGATGGAAGAACTGGGAATGCCCCCTGCTGAGCCACCCAGGGTGCATG 510
Qy      412  CCGGCTTCCGCTCTGCTTTCAGCGGGGAGAGGGTCTAGTTGGCTCCCATCTG 471
Db      511  CCGGCTTCCGCTCTGCTTTCAGCGGGGAGAGGGTCTAGTTGGCTCCCATCTG 570
Qy      472  CAGAGCTTCCGAGAGTGTCTGCTACCGGCTTCTAGCCACCTTGCCAGCCCT 523
Db      571  CAGAGCTTCCGAGAGTGTCTGCTACCGGCTTCTAGCCACCTTGCCAGCCCT 622

RESULT 10
BM915836
LOCUS   993 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6639697 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482095
5', mRNA sequence.
ACCESSION BM915836
VERSION   1
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 993)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/BTP
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: L1CM2007 row: j column: 16
          High quality sequence start: 17
          High quality sequence stop: 711.
          Location/Qualifiers
            1..993
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5482095"
              /tissue_type="amelanotic melanoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH MGC 41"
              /note="organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dT priming. Directionally cloned
              into EcoRI/XhoI sites using the following 5' adaptor:
              GGCACGAG(G). Library constructed by Ling Hong in the
              Laboratory of Gerald M. Rubin (University of California,
              Berkeley) using 5AP-cDNA synthesis kit (Stratagene) and
              Superscript II RT (Life Technologies). Note: this is a
              NIH_MGC Library."

FEATURES
source
    Query Match 95.5%; Score 499.4; DB 12; Length 993;
    Best Local Similarity 99.4%; Pred. No. 5.2e-92;
    Matches 522; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy      1  ACCCCCTGGGCGCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
Db      295  ACCCCCTGGGCGCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 354
Qy      61  GTGAGGAAGATCCAGGGCGATGGCGCAGCGTTCAGGAGAGCTGTGTGCCACCTACAAG 120

```

```

Db      355  GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAAGCTGTGTGCCACCTACAAG 414
Qy      121  CTGTGCCACCCGAGAGAGCTGTGTGTCTGCGACACTCTCTGGGCATCCCTGGGCTCCC 180
Db      415  CTGTGCCACCCGAGAGAGCTGTGTGTCTGCGACACTCTCTGGGCATCCCTGGGCTCCC 474
Qy      181  CTGAGCAGCTGCCCCAGCAGCGCCCTGAGCTGGCAGGCTGCTTGGAGCAACTCCATAGC 240
Db      475  CTGAGCAGCTGCCCCAGCAGCGCCCTGAGCTGGCAGGCTGCTTGGAGCAACTCCATAGC 534
Qy      241  GGCCTTTTCTCTACAGGGGCTCTGAGGCGCTTGGAGGCTTGGAGGATCTCCCGAGTTGGT 300
Db      535  GGCCTTTTCTCTACAGGGGCTCTGAGGCGCTTGGAGGCTTGGAGGATCTCCCGAGTTGGT 594
Qy      301  CCCACCTTGGACACACTGCGAGCTGCGCGACTTTGCCACCAACCATCTGGCAGCAG 360
Db      595  CCCACCTTGGACACACTGCGAGCTGCGCGACTTTGCCACCAACCATCTGGCAGCAG 654
Qy      361  ATGGAAGAACTGGGAATGG-CCCTGCGCTTGAGCCACCTTGGCCAGGCCCT 523
Db      655  ATGGAAGAACTGGGAATGGCCCTGCGCTTGAGCCACCTTGGCCAGGCCCT 819
Qy      419  TCGCCTCTGCTTTCAGCGCGGGGAGGAGGGTCTAGTTGCCCTCCCATCTGCAGAGCT 478
Db      715  TCGCCTCTGCTTTCAGCGCGGGGAGGAGGGTCTAGTTGCCCTCCCATCTGCAGAGCT 774
Qy      479  TCGTGGAGGTGTCGTACCGCGCTTTCAGCGCACCTTGGCCAGGCCCT 523
Db      775  TCGTGGAGGTGTCGTACCGCGCTTTCAGCGCACCTTGGCCAGGCCCT 819

RESULT 11
AY414901
LOCUS   608 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes CSF3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY414901
VERSION   1
KEYWORDS GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 608)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
          Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
          Science 302 (5652), 1960-1963 (2003)
          14671302
JOURNAL   Science 302 (5652), 1960-1963 (2003)
REFERENCE 2 (bases 1 to 608)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
          Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
          Location/Qualifiers
            1..608
              /organism="Pan troglodytes"
              /mol_type="genomic DNA"
              /db_xref="taxon:9598"
              <1..>608
              /gene="CSF3"
              /locus_tag="HCM5378"

ORIGIN
    Query Match 95.1%; Score 497.6; DB 29; Length 608;

```

```

Best Local Similarity 97.6%; Pred. No. 9,7e-92;
Matches 519; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

QY 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 60
   |||||
Db 75 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 134
   |||||
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCT-----GTGTGCC 111
   |||||
Db 135 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGGTGAAGTGTGTGCC 194
   |||||
QY 112 ACCTACAAGCTGTGCCACCCCGAGAGAGCTGTGTCTCGGACACTCTCTGGGCATCCCC 171
   |||||
Db 195 ACCTACAAGCTGTGCCACCCCGAGAGAGCTGTGTCTCGGACACTCTCTGGGCATCCCC 254
   |||||
QY 172 TGGGCTCCCTGAGGAGCTGCCCCAGCAGCGCCCTGCAGCTGGCAGGCTGTAGAGCAA 231
   |||||
Db 255 TGGGCTCCCTGAGCAGCTGCCCCAGCAGCGCCCTGCAGCTGGCAGGCTGTAGAGCAA 314
   |||||
QY 232 CTCCTATAGCGGCTTTCTCTTACACAGGGGCTCTCTGCAGGCGCTCGAAGGGATCTCCCC 291
   |||||
Db 315 CTCCTATAGCGGCTTTCTCTTACACAGGGGCTCTCTGCAGGCGCTCGAAGGGATCTCCCC 374
   |||||
QY 292 GAGTTGGTCCCACTTGGACACACTGAGCTGGAGCTGCGCGACTTTGCCACCAACATC 351
   |||||
Db 375 GAGTTGGTCCCACTTGGACACACTGAGCTGGAGCTGCGCGACTTTGCCACCAACATC 434
   |||||
QY 352 TGCACGACATGAGAACTGGGAATGGCCCTGCGCCCTGCAGCCACCCAGGCTGCCATG 411
   |||||
Db 435 TGCACGACATGAGAACTGGGAATGGCCCTGCGCCCTGCAGCCACCCAGGCTGCCATG 494
   |||||
QY 412 CCGGCTTCGCTCTCTTCCAGCGCCGGGAGGAGGGTCTTAGTTCCTCCCATCTG 471
   |||||
Db 495 CCGGCTTCGCTCTCTTCCAGCGCCGGGAGGAGGGTCTTAGTTCCTCCCATCTG 554
   |||||
QY 472 CAGAGCTTCCTGAGGTGCTGACCGGTTCTACCGCACTTGCACCGCTTGCACCGCTT 523
   |||||
Db 555 CAGAGCTTCCTGAGGTGCTGACCGGTTCTACCGCACTTGCACCGCTTGCACCGCTT 606
   |||||

RESULT 12
BM423896 990 bp mRNA linear EST 29-JAN-2002
AGENCOURT_6399123 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5517129
5', mRNA sequence.
BM423896
BM423896.1 GI:18392108
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2018 row: n column: 10
High quality sequence stop: 542.
Location/Qualifiers
1..990
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5517129"

FEATURES
source

```

```

/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 93.6%; Score 489.4; DB 12; Length 990;
Best Local Similarity 97.1%; Pred. No. 5.8e-90;
Matches 507; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 60
   |||||
Db 271 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 330
   |||||
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGCGCACTACAA 120
   |||||
Db 331 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGCGCACTACAA 390
   |||||
QY 121 CTGTGCCACCCCGAGGAGCTGTGTCTGCTCGGACACTCTCTGGGCACTCCCTGGGCTCCC 180
   |||||
Db 391 CTGTGCCACCCCGAGGAGCTGTGTCTGCTCGGACACTCTCTGGGCACTCCCTGGGCTCCC 450
   |||||
QY 181 CTGAGCAGCTGCCCGAGGAGCTGTGTCTGCTCGGAGCTGTGAGCCAACTCCATAG 240
   |||||
Db 451 CTGAGCAGCTGCCCGAGGAGCTGTGTCTGCTCGGAGCTGTGAGCCAACTCCATAG 510
   |||||
QY 241 GGCCTTTTCTCTACACAGGGGCTCTCTGAGGCGCTTGAAGGGATCTCCCGGAGTTGGT 300
   |||||
Db 511 GGCCTTTTCTCTACACAGGGGCTCTCTGAGGCGCTTGAAGGGATCTCCCGGAGTTGGT 570
   |||||
QY 301 CCACCTTGGACACACTGAGCTGAGCTGCGGAGCTTTGCCACACCACTCTGGGAGCAG 360
   |||||
Db 571 CCACCTTGGACACACTGAGCTGAGCTGCGGAGCTTTGCCACACCACTCTGGGAGCAG 630
   |||||
QY 361 ATCGAAGAACTGGGAATGCGCCCTGCGCCCTGCAGCCACCCAGGCTGCCATCGCGCTTC 420
   |||||
Db 631 ATCGAAGAACTGGGAATGCGCCCTGCGCCCTGCAGCCACCCAGGCTGCCATCGCGCTTC 690
   |||||
QY 421 GCCTCTGCTTTCCAGCGCGGGG-AGGAGGGGTCTTAGTTGCTCCCATCTGCGAGCTTT 479
   |||||
Db 691 GNCTCTGCTTTCCAGCGCGGGGCAAGAGGGGTCTGTTGGCTCTCCATCTGCGAGCTT 750
   |||||
QY 480 CTGAGGAGTGTCTGCTACCGGTTCTAGCGCACCTTGGCCAGCC 521
   |||||
Db 751 CTGAGGAGTGTCTGCTACCGGTTCTAGCGCACCTTGGCCAGCC 792
   |||||

CA487515 986 bp mRNA linear EST 14-NOV-2002
AGENCOURT_10809149 MAPcL Homo sapiens cDNA clone IMAGE:6719006 5',
mRNA sequence.
CA487515
CA487515.1 GI:24947095
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan

```

cdNA Library Preparation: Invitrogen Corp
 cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM14276 row: d column: 14
 High quality sequence stop: 562.
 Location/Qualifiers
 1. 986
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6719006"
 /cell_line="2E-75-1, MCF7, SK-BR-3, MDA-MB-231,
 hTERT-HME1, LNCaP"
 /lab_host="EMDH10B"
 /clone_lib="WAPC1"
 /note="Vector: pCMV-Sport6; Site 1: EcoRV; Site 2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dt. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Buckook Lee & Ira Pastan. Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

ORIGIN

Query Match 92.8%; Score 485.6; DB 14; Length 986;
 Best Local Similarity 97.9%; Pred. No. 3.5e-89;
 Matches 513; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
 QY 1 ACCCCCTGGCCCTGCAGCTCCCTGCCCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
 DB 285 ACCCCCTGGCCCTGCAGCTCCCTGCCCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 344
 QY 61 GTGAGGAGATCCAGGGCGATGGCGCAGCGCTCCAGAGAGCTGTGTGCCACTACAAG 120
 DB 345 GTGAGGAGATCCAGGGCGATGGCGCAGCGCTCCAGAGAGCTGTGTGCCACTACAAG 404
 QY 121 CTGTGCCACCCGAGGAGCTGGTGTCTGTGGACACTCTCTGGGCATCCCTGGGCTCC 180
 DB 405 CTGTGCCACCCGAGGAGCTGGTGTCTGTGGACACTCTCTGGGCATCCCTGGGCTCC 464
 QY 181 CTGAGCAGCTGCCCGCCAGCGCTCCAGCTGAGCTGTGAGCCAACTCCATAGC 240
 DB 465 CTGAGCAGCTGCCCGCCAGCGCTCCAGCTGAGCTGTGAGCCAACTCCATAGC 524
 QY 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGG - CCTTGAAGGATCTCCCCCGAGTTGGG 299
 DB 525 GGCCTTTTCTCTACAGGGGCTCTCTGAGG - CCTTGAAGGATCTCCCCCGAGTTGGG 584
 QY 300 TCCACCTTGGACACATGAGCTGGAGCTGCGGAGCTTTGCCACACCATCTGGCAGCA 359
 DB 585 TCCACCTTGGACACATGAGCTGGAGCTGCGGAGCTTTGCCACACCATCTGGCAGCA 644
 QY 360 GATGAAGAACTGGGAATGGCCCTCTCCCTCAGCCACCCAGGGTGCATGCCGGCTT 419
 DB 645 GATGAAGAACTGGGAATGGCCCTCTCCCTCAGCCACCCAGGGTGCATGCCGGCTT 704
 QY 420 CCGCTCTCTTCCAGCGCCCGGAGAGGGGTCTAGTTGCCCTCCCATCTGACAGCTT 479
 DB 705 CCGCTCTCTT - CAGCGCCCGGAGAGGGGTCTAGTTGCCCTCCCATCTGCAAGCTTT 763
 QY 480 CTTGAGAGTGTGTAACCGGTTCTACGCCACCTTTGCCAGCCCT 523
 DB 764 CTTGAGAGTGTGTAACCGGTTCTACGCCACCTTTGCCAGCCCT 807

RESULT 14

BM556479 1012 bp mRNA linear EST 20-FEB-2002
 LOCUS AGENCOURT_6578168 NIH_MGC_41 Homo sapiens cdNA clone IMAGE:5467332
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

5', mRNA sequence.
 BM556479
 BM556479.1 GI:18797743
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1012)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cdNA Library Preparation: Rubin Laboratory
 cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM1969 row: c column: 13
 High quality sequence stop: 19
 High quality sequence stop: 745.

FEATURES
 Location/Qualifiers
 1..1012
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5467332"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 41"
 /note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cdNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 92.4%; Score 483; DB 12; Length 1012;
 Best Local Similarity 97.5%; Pred. No. 1.2e-88;
 Matches 512; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
 QY 1 ACCCCCTGGCCCTGCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTCTTAGAGCAA 60
 DB 298 ACCCCCTGGCCCTGCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTCTTAGAGCAA 357
 QY 61 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACTACAAG 120
 DB 358 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACTACAAG 417
 QY 121 CTGTGCCACCCGAGGAGCTGGTGTCTGTGGACACTCTCTGGGATCCCTGGGCTCC 180
 DB 418 CTGTGCCACCCGAGGAGCTGGTGTCTGTGGACACTCTCTGGGATCCCTGGGCTCC 477
 QY 181 CTGAGCAGCTGCCCGCCAGCGCTGCGAGCTGGAGGCTGTGAGCCAACTCCATAGC 240
 DB 478 CTGAGCAGCTGCCCGCCAGCGCTGCGAGCTGGAGGCTGTGAGCCAACTCCATAGC 537
 QY 241 GGCCTTTTCTCTTACCCAGGGGCTCTCTGAGGCGCTTGAAGGATCTCCCCAGTTGGT 300
 DB 538 GGCCTTTTCTCTTACCCAGGGGCTCTCTGAGGCGCTTGAAGGATCTCCCCAGTTGGT 597
 QY 301 CCCACCTTGGACACACTGAGCTGGACCTGCGGACTTTGCCACCACTCTGGGAGCAG 360
 DB 598 CCCACCTTGGACACACTGAGCTGGACCTGCGGACTTTGCCACCACTCTGGGAGCAG 657
 QY 361 ATGCAAGAACTGGGAATGCCCTTGCCTGCGAGCCACCCAGGGTGCATGCCGCGCTTC 420

Db 658 ATGGAAGAACTGGGAATGCCCTGCCCTGCAGCCACCCAGGGTGCCATGCCGSCCTTC 717
 QY 421 GCTCTGCTTCCAGCGCGGG--CAGGAGGGGTCTAGTTGCTTCCCTCCATCTGCAGAGCT 478
 Db 718 GCTCTGCTTCCAGCGCGGGGAGGAGGGGTCTGTTGCTTCCCTCCATCTGCAAGCTT 777
 QY 479 TCTT-GGAGGTGCTGCTACCGCTTCTACGCCACCTTGCCCGAGCC 522
 Db 778 TCTGCGAGGTTTGGTACCGGCTTCTACGCCACCTTGCCCGAGCC 822

RESULT 15
 CB126975 554 bp mRNA linear EST 29-JAN-2003
 LOCUS K-EST0176151 C1SNU17 Homo sapiens cDNA clone C1SNU17-14-A07 5',
 DEFINITION mRNA sequence.
 ACCESSION CB126975
 VERSION 1
 KEYWORDS CB126975.1 GI:28089170
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 554)
 AUTHORS Kim,N.S., Kahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 14 row: A column: 07
 High quality sequence stop: 554.
 Location/Qualifiers

FEATURES
 source
 1..554
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C1SNU17-14-A07"
 /sex="F"
 /tissue_type="uterine"
 /cell_type="Epithelial"
 /cell_line="SNU-17"
 /lab_host="Top10F"
 /clone_lib="C1SNU17"
 /note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then deapped
 with tabacco acid pyrophosphatase (TAP). The deapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 81.5%; Score 426; DB 14; Length 554;
 Best Local Similarity 100.0%; Pred.No. 4.3e-77;
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCCCTGGGCGCTGCCAGCTCCCTGCCCGCAGAGCTTCTCTCAAGTGCTTAGACAA 60

Db 129 ACCCCCTGGGCGCTGCCAGCTCCCTGCCCGCAGAGCTTCTCTCAAGTGCTTAGACAA 188
 QY 61 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120
 Db 189 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 248
 QY 121 CTGTGCCACCCCGAGGAGCTGTGTGCTGCTCGGACACTCTCTCTGGGCATCCCTGGGCTCCC 180
 Db 249 CTGTGCCACCCCGAGGAGCTGTGTGCTGCTCGGACACTCTCTCTGGGCATCCCTGGGCTCCC 308
 QY 181 CTGAGCAGCTGCCCGCAGCCAGCCCTGCAGCTGGCAGGCTGCTTGAGCCCACTCCATAGC 240
 Db 309 CTGAGCAGCTGCCCGCAGCCAGCCCTGCAGCTGGCAGGCTGCTTGAGCCCACTCCATAGC 368
 QY 241 GGCTTTTCTCTTACCAGGGGCTCTCTGCAGGGCTTGGAAAGGGATCTCCCCCGAGTTGGGT 300
 Db 369 GGCTTTTCTCTTACCAGGGGCTCTCTGCAGGGCTTGGAAAGGGATCTCCCCCGAGTTGGGT 428
 QY 301 CCCACCTTGGACACACTGCAGCTGGACGTGCGCGACTTTGCCACACACATCTGGCAGCAG 360
 Db 429 CCCACCTTGGACACACTGCAGCTGGACGTGCGCGACTTTGCCACACACATCTGGCAGCAG 488
 QY 361 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCACCCAGGCTGCCATGCCGCGCTTC 420
 Db 489 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCACCCAGGCTGCCATGCCGCGCTTC 548
 QY 421 GCCTCT 426
 Db 549 GCCTCT 554

Search completed: October 9, 2004, 04:22:26
 Job time : 3235.76 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 03:08:44 ; Search time 449.349 Seconds
(without alignments)
5900.506 Million cell updates/sec

Title: US-10-009-792C-18_COPY_88_610

Perfect score: 523
Sequence: 1 acccccctggccctgcag.....acgccacctggccagccct 523

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US0C_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	100.0	531	15	US-10-009-792A-20
2	523	100.0	615	15	US-10-009-792A-18
3	523	100.0	630	13	US-10-609-346-17
4	523	100.0	1498	12	US-10-447-315-18
5	523	100.0	2352	13	US-10-609-346-7
6	522	99.8	1365	10	US-09-968-362-21
7	522	99.8	1368	10	US-09-968-362-17
8	522	99.8	1371	10	US-09-968-362-19
9	521.4	99.7	525	13	US-10-411-037-1
10	521.4	99.7	525	13	US-10-411-026-1
11	521.4	99.7	525	17	US-10-410-962-1
12	521.4	99.7	525	17	US-10-411-049-1
13	521.4	99.7	525	17	US-10-410-930-1
14	521.4	99.7	525	17	US-10-410-997-1

15	521.4	99.7	525	17	US-10-411-012-1	Sequence 1, Appli
16	521.4	99.7	525	17	US-10-287-994-1	Sequence 1, Appli
17	521.4	99.7	525	17	US-10-410-913-1	Sequence 1, Appli
18	521.4	99.7	1508	14	US-10-044-090-825	Sequence 825, App
19	521.4	99.7	1703	12	US-10-447-315-22	Sequence 22, Appl
20	510.2	97.6	541	9	US-09-984-186-13	Sequence 13, Appl
21	510.2	97.6	541	15	US-10-237-667-13	Sequence 13, Appl
22	510.2	97.6	541	15	US-10-237-708-13	Sequence 13, Appl
23	510.2	97.6	541	15	US-10-237-866-13	Sequence 13, Appl
24	510.2	97.6	541	15	US-10-237-871-13	Sequence 13, Appl
25	510.2	97.6	541	15	US-10-237-624-13	Sequence 13, Appl
26	510.2	97.6	541	17	US-10-702-536-13	Sequence 13, Appl
27	510.2	97.6	541	17	US-10-702-636-13	Sequence 13, Appl
28	509.2	97.4	2455	9	US-09-984-186-15	Sequence 15, Appl
29	509.2	97.4	2455	15	US-10-237-667-15	Sequence 15, Appl
30	509.2	97.4	2455	15	US-10-237-708-15	Sequence 15, Appl
31	509.2	97.4	2455	15	US-10-237-866-15	Sequence 15, Appl
32	509.2	97.4	2455	15	US-10-237-871-15	Sequence 15, Appl
33	509.2	97.4	2455	15	US-10-237-624-15	Sequence 15, Appl
34	509.2	97.4	2455	17	US-10-702-536-15	Sequence 15, Appl
35	509.2	97.4	2455	17	US-10-702-636-15	Sequence 15, Appl
36	503.8	96.3	546	15	US-10-083-446-177	Sequence 177, App
37	503.8	96.3	521	15	US-10-083-446-72	Sequence 72, Appl
38	503.8	96.3	921	15	US-10-083-446-75	Sequence 75, Appl
39	503.8	96.3	921	15	US-10-083-446-78	Sequence 78, Appl
40	503.8	96.3	966	15	US-10-083-446-73	Sequence 73, Appl
41	503.8	96.3	966	15	US-10-083-446-77	Sequence 77, Appl
42	503.8	96.3	966	15	US-10-083-446-79	Sequence 79, Appl
43	503.8	96.3	1047	15	US-10-083-446-74	Sequence 74, Appl
44	503.8	96.3	1047	15	US-10-083-446-76	Sequence 76, Appl
45	502.8	96.1	921	15	US-10-083-446-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1

US-10-009-792A-20
; Sequence 20, Application US/10009792A
; Publication No. US20030153049A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; APPLICANT: JESONG, Ki-Jun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; FILE REFERENCE: HYLEB60.001APC
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-792A-20

Query Match	100.0%	Score 523	DB 15	Length 531
Best Local Similarity	100.0%	Pred. No. 1.6e-133		
Matches 523	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	ACCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA	60	
Db	4	ACCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA	63	
Qy	61	GTGAGGAGATCCAGGGCGATGCGCAGAGCTCCAGAGAGCTGTGTGCCACTCAAG	120	
Db	64	GTGAGGAGATCCAGGGCGATGCGCAGAGCTCCAGAGAGCTGTGTGCCACTCAAG	123	
Qy	121	CTGTGTCACCCCGAGGAGCTGTGTGCTCTCGGACACTCTCTGGGCATCCCTGGGTCC	180	

Qy	421	GCCTCTGCTTTTCACGGCGCGGACGAGGGGTCTAGTTCCTTCCCATCTGCAGAGCTTC	480
Db	517	GCCTCTGCTTTTCACGGCGCGGACGAGGGGTCTAGTTCCTTCCCATCTGCAGAGCTTC	576
Qy	481	CTGAGGGTCTGATACGGGTCTTACGCCACCTTCCCGAGCCT	523
Db	577	CTGAGGGTCTGATACGGGTCTTACGCCACCTTCCCGAGCCT	619

RESULT 4

```

US-10-447-315-18
; Sequence 18, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heissig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-447-315-18

```

RESULT 5

```

US-10-609-346-7
:
: Sequence 7, Application US/10609346
: Publication No. US2004008635A1
: GENERAL INFORMATION:
: APPLICANT: Yu, Zailin
: APPLICANT: Fu, Yan
: TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LAST
: TITLE OF INVENTION: EFFECTS
: FILE REFERENCE: ZYU-0603
: CURRENT APPLICATION NUMBER: US/10/609,346
: CURRENT FILING DATE: 2003-06-26
: PRIOR APPLICATION NUMBER: US 60/392,948
: PRIOR FILING DATE: 2002-07-01
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 7
: LENGTH: 2352
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: DNA of HSA-GCSF
US-10-609-346-7

```

RESULT 6

US-09-988-362-21
; Sequence 21, Application US/09968362
; Publication No. US2003082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill

; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma1 (Figure 2C)
US-09-968-362-21

Query Match 99.8%; Score 522; DB 10; Length 1365;
Best Local Similarity 100.0%; Pred. No. 3.2e-133;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
DB 106 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 165
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
DB 166 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 225
QY 121 CTGTGCCACCCGAGAGCTGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 226 CTGTGCCACCCGAGAGCTGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 285
QY 181 CTGAGCAGCTGCCCCAGAGCGCTTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
DB 286 CTGAGCAGCTGCCCCAGAGCGCTTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 345
QY 241 GGCCTTTTCTCTACAGGGGCTCTCGAGGCGCTTGGAGGATCTCTCCCGAGTTGGGT 300
DB 346 GGCCTTTTCTCTACAGGGGCTCTCGAGGCGCTTGGAGGATCTCTCCCGAGTTGGGT 405
QY 301 CCCACCTTGGACACACTGACAGCTGGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 360
DB 406 CCCACCTTGGACACACTGACAGCTGGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 465
QY 361 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCCACCCAGGGTGCCATGCCGCTTC 420
DB 466 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCCACCCAGGGTGCCATGCCGCTTC 525
QY 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGCTCTAGTTCCTCCATCTGAGAGCTTC 480
DB 526 GCCTCTGCTTTCCAGCGCCGGGAGGAGGCTCTAGTTCCTCCATCTGAGAGCTTC 585
QY 481 CTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCAGGCC 522
DB 586 CTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCAGGCC 627

RESULT 7

US-09-968-362-17
; Sequence 17, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Lee-Hwei K
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17

; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma2 (Figure 2A)
US-09-968-362-17

Query Match 99.8%; Score 522; DB 10; Length 1368;
Best Local Similarity 100.0%; Pred. No. 3.2e-133;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
DB 106 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 165
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
DB 166 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 225
QY 121 CTGTGCCACCCGAGAGCTGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 226 CTGTGCCACCCGAGAGCTGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 285
QY 181 CTGAGCAGCTGCCCCAGAGCGCTTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
DB 286 CTGAGCAGCTGCCCCAGAGCGCTTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 345
QY 241 GGCCTTTTCTCTACAGGGGCTCTCGAGGCGCTTGGAGGATCTCTCCCGAGTTGGGT 300
DB 346 GGCCTTTTCTCTACAGGGGCTCTCGAGGCGCTTGGAGGATCTCTCCCGAGTTGGGT 405
QY 301 CCCACCTTGGACACACTGACAGCTGGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 360
DB 406 CCCACCTTGGACACACTGACAGCTGGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 465
QY 361 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCCACCCAGGGTGCCATGCCGCTTC 420
DB 466 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCCACCCAGGGTGCCATGCCGCTTC 525
QY 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGCTCTAGTTCCTCCATCTGAGAGCTTC 480
DB 526 GCCTCTGCTTTCCAGCGCCGGGAGGAGGCTCTAGTTCCTCCATCTGAGAGCTTC 585
QY 481 CTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCAGGCC 522
DB 586 CTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCAGGCC 627

RESULT 8

US-09-968-362-19
; Sequence 19, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hG-CSF-L-vFc gamma4 (Figure 2B)
US-09-968-362-19

Query Match 99.8%; Score 522; DB 10; Length 1371;
Best Local Similarity 100.0%; Pred. No. 3.2e-133;

;; PRIOR FILING DATE: 2002-08-16
;; PRIOR APPLICATION NUMBER: US 60/407,527
;; PRIOR FILING DATE: 2002-08-28
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: Patent in version 3.2
;; SEQ ID NO 1
;; LENGTH: 525
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-411-026-1

Query Match 99.7%; Score 521.4; DB 13; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-133;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCCCTGGGCGCTCCAGAGTCCCTGCCCCAGAGTTCCTGCTCAAGTGTCTTAGAGCAA 60
DB 1 ACCCCCCCTGGGCGCTCCAGAGTCCCTGCCCCAGAGTTCCTGCTCAAGTGTCTTAGAGCAA 60

QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTTACAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTTACAAG 120

QY 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGACACTCTCTGGGCATCCCTGGGCTCCC 180

QY 181 CTGAGCAGTGCCTCCAGCCAGAGCTGTGTGCTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
DB 181 CTGAGCAGTGCCTCCAGCCAGAGCTGTGTGCTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240

QY 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGGCTTGGAAAGGATCTCTCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGGCTTGGAAAGGATCTCTCCCGAGTTGGGT 300

QY 301 CCACCTTGGACACACTGACGTGGAGCTGGCGAGCTTGGCCACCACTTGGCAGCAG 360
DB 301 CCACCTTGGACACACTGACGTGGAGCTGGCGAGCTTGGCCACCACTTGGCAGCAG 360

QY 361 ATGGAAGAATGGGAATGGCCCTGCGCTCGAGCCACCCAGGCTGCCATGCCGCTTC 420
DB 361 ATGGAAGAATGGGAATGGCCCTGCGCTCGAGCCACCCAGGCTGCCATGCCGCTTC 420

QY 421 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTAGTTGCTCCCATCTGCAAGCTTC 480
DB 421 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTAGTTGCTCCCATCTGCAAGCTTC 480

CTGGAGGTGTCGTACCGCGTTCACGCCACCTTGGCCAGCCCT 523
CTGGAGGTGTCGTACCGCGTTCACGCCACCTTGGCCAGCCCT 523

RESULT 11
US-10-410-962-1
; Sequence 1, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US 60/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19

;; PRIOR APPLICATION NUMBER: US 60/387,292
;; PRIOR FILING DATE: 2002-06-07
;; PRIOR APPLICATION NUMBER: US 60/391,777
;; PRIOR FILING DATE: 2002-06-25
;; PRIOR APPLICATION NUMBER: US 60/396,594
;; PRIOR FILING DATE: 2002-07-17
;; PRIOR APPLICATION NUMBER: US 60/404,249
;; PRIOR FILING DATE: 2002-08-16
;; PRIOR APPLICATION NUMBER: US 60/407,527
;; PRIOR FILING DATE: 2002-08-28
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: Patent in version 3.2
;; SEQ ID NO 1
;; LENGTH: 525
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-410-962-1

Query Match 99.7%; Score 521.4; DB 17; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-133;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCCCTGGGCGCTCCAGAGTCCCTGCCCCAGAGTTCCTGCTCAAGTGTCTTAGAGCAA 60
DB 1 ACCCCCCCTGGGCGCTCCAGAGTCCCTGCCCCAGAGTTCCTGCTCAAGTGTCTTAGAGCAA 60

QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTTACAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTTACAAG 120

QY 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGACACTCTCTGGGCATCCCTGGGCTCCC 180

QY 181 CTGAGCAGTGCCTCCAGCCAGAGCTGTGTGCTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
DB 181 CTGAGCAGTGCCTCCAGCCAGAGCTGTGTGCTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240

QY 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGGCTTGGAAAGGATCTCTCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGGCTTGGAAAGGATCTCTCCCGAGTTGGGT 300

QY 301 CCACCTTGGACACACTGACGTGGAGCTGGCGAGCTTGGCCACCACTTGGCAGCAG 360
DB 301 CCACCTTGGACACACTGACGTGGAGCTGGCGAGCTTGGCCACCACTTGGCAGCAG 360

QY 361 ATGGAAGAATGGGAATGGCCCTGCGCTCGAGCCACCCAGGCTGCCATGCCGCTTC 420
DB 361 ATGGAAGAATGGGAATGGCCCTGCGCTCGAGCCACCCAGGCTGCCATGCCGCTTC 420

QY 421 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTAGTTGCTCCCATCTGCAAGCTTC 480
DB 421 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTAGTTGCTCCCATCTGCAAGCTTC 480

CTGGAGGTGTCGTACCGCGTTCACGCCACCTTGGCCAGCCCT 523
CTGGAGGTGTCGTACCGCGTTCACGCCACCTTGGCCAGCCCT 523

RESULT 12
US-10-411-049-1
; Sequence 1, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US 60/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19

FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patent in version 3.2
SEQ ID NO 1
LENGTH: 525
TYPE: DNA
ORGANISM: Homo sapiens
US-10-411-049-1

Query Match 99.7%; Score 521.4; DB 17; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-133;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTGCTCAAGTGTAGAGCAA 60
DB 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTGCTCAAGTGTAGAGCAA 60

QY 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120

QY 121 CTGTGCCACCCGAGAGCTGTGTGTGTGGACACTCTGTGGGATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCGAGAGCTGTGTGTGTGGACACTCTGTGGGATCCCTGGGCTCCC 180

QY 181 CTGACAGCTGCCCGAGCGCTCCAGCGCTGAGCTGGGAGGCTGTGTGAGCAACTCCATAGC 240
DB 181 CTGACAGCTGCCCGAGCGCTCCAGCGCTGAGCTGGGAGGCTGTGTGAGCAACTCCATAGC 240

QY 241 GGCCTTTTCTTACAGGGGCTCTGTGAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTTACAGGGGCTCTGTGAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300

QY 301 CCCACCTTGGACACTGACGTGACCTGCGCGACTTTGCGACCACTCCACCATCTGGCAGCAG 360
DB 301 CCCACCTTGGACACTGACGTGACCTGCGCGACTTTGCGACCACTCCACCATCTGGCAGCAG 360

QY 361 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGGTGCCATCCCGGCTTC 420
DB 361 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGGTGCCATCCCGGCTTC 420

QY 421 GCCTCTGCTTCCAGCGCGGAGAGGGTCTGTAGTTGCTTCCATCTGCAAGCTTC 480
DB 421 GCCTCTGCTTCCAGCGCGGAGAGGGTCTGTAGTTGCTTCCATCTGCAAGCTTC 480

QY 481 CTGGAGGTGTCTACCGGGTCTACGCCACCTTGGCCAGCCCT 523
DB 481 CTGGAGGTGTCTACCGGGTCTACGCCACCTTGGCCAGCCCT 523

RESULT 13
US-10-410-930-1
Sequence 1, Application US/10410930
Publication No. US20040115168A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn

APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5056
CURRENT APPLICATION NUMBER: US/10/410,930
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patent in version 3.2
SEQ ID NO 1
LENGTH: 525
TYPE: DNA
ORGANISM: Homo sapiens
US-10-410-930-1

Query Match 99.7%; Score 521.4; DB 17; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-133;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTGCTCAAGTGTAGAGCAA 60
DB 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCGAGAGCTTCTGCTCAAGTGTAGAGCAA 60

QY 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120

QY 121 CTGTGCCACCCGAGAGCTGTGTGTGTGGACACTCTGTGGGATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCGAGAGCTGTGTGTGTGGACACTCTGTGGGATCCCTGGGCTCCC 180

QY 181 CTGACAGCTGCCCGAGCGCTCCAGCGCTGAGCTGGGAGGCTGTGTGAGCAACTCCATAGC 240
DB 181 CTGACAGCTGCCCGAGCGCTCCAGCGCTGAGCTGGGAGGCTGTGTGAGCAACTCCATAGC 240

QY 241 GGCCTTTTCTTACAGGGGCTCTGTGAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTTACAGGGGCTCTGTGAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300

QY 301 CCCACCTTGGACACTGACGTGACCTGCGCGACTTTGCGACCACTCCACCATCTGGCAGCAG 360
DB 301 CCCACCTTGGACACTGACGTGACCTGCGCGACTTTGCGACCACTCCACCATCTGGCAGCAG 360

QY 361 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGGTGCCATCCCGGCTTC 420
DB 361 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGGTGCCATCCCGGCTTC 420

QY 421 GCCTCTGCTTCCAGCGCGGAGAGGGTCTGTAGTTGCTTCCATCTGCAAGCTTC 480
DB 421 GCCTCTGCTTCCAGCGCGGAGAGGGTCTGTAGTTGCTTCCATCTGCAAGCTTC 480

QY 481 CTGGAGGTGTCTACCGGGTCTACGCCACCTTGGCCAGCCCT 523
DB 481 CTGGAGGTGTCTACCGGGTCTACGCCACCTTGGCCAGCCCT 523

RESULT 14
US-10-410-997-1
; Sequence 1, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePress, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; TITLE OF INVENTION: FSH
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/397,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-997-1

Query Match 99.7%; Score 521.4; DB 17; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-133;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
Db 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60

Qy 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGTGTGTGCTCAAGTCTTAGAGCAA 120
Db 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGTGTGTGCTCAAGTCTTAGAGCAA 120

Qy 121 CTGTGCCACCCCGAGGAGTGTGTGTGCTCGGACACTCTCTGGGCAATCCCTGGGCTCCC 180
Db 121 CTGTGCCACCCCGAGGAGTGTGTGTGCTCGGACACTCTCTGGGCAATCCCTGGGCTCCC 180

Qy 181 CTGAGCAGCTGCCCCAGCCAGGCGCTCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 240
Db 181 CTGAGCAGCTGCCCCAGCCAGGCGCTCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 240

Qy 241 GGCCTTTTCTCTACAGGGGCTCCCTGCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300
Db 241 GGCCTTTTCTCTACAGGGGCTCCCTGCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300

Qy 301 CCCACCTTGAGACACTGAGCTGGAGCTGCCGACTTTGCCACCACTCTGGCAGCAG 360
Db 301 CCCACCTTGAGACACTGAGCTGGAGCTGCCGACTTTGCCACCACTCTGGCAGCAG 360

Qy 361 ATGGAAGAACTGGGAATGGCCCTGCTGCACGCCACCCAGGGTCCCATGCGGCTTTC 420
Db 361 ATGGAAGAACTGGGAATGGCCCTGCTGCACGCCACCCAGGGTCCCATGCGGCTTTC 420

Qy 421 GCCTCTGCTTTCCAGGCGCGGGCAGGAGGGTCTTAGTTGCTTCCCATCTGAGAGCTTC 480
Db 421 GCCTCTGCTTTCCAGGCGCGGGCAGGAGGGTCTTAGTTGCTTCCCATCTGAGAGCTTC 480

Db 421 GCCTCTGCTTTCCAGGCGCGGGCAGGAGGGTCTTAGTTGCTTCCCATCTGAGAGCTTC 480

Qy 481 CTGAGAGTGTCTACCGCTTCTACCGCCACCTTGCCAGCCCT 523
Db 481 CTGAGAGTGTCTACCGCTTCTACCGCCACCTTGCCAGCCCT 523

RESULT 15
US-10-411-012-1
; Sequence 1, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePress, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GLYCOPEPSYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-012-1

Query Match 99.7%; Score 521.4; DB 17; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-133;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
Db 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60

Qy 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGTGTGTGCTCAAGTCTTAGAGCAA 120
Db 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGTGTGTGCTCAAGTCTTAGAGCAA 120

Qy 121 CTGTGCCACCCCGAGGAGTGTGTGTGCTCGGACACTCTCTGGGCAATCCCTGGGCTCCC 180
Db 121 CTGTGCCACCCCGAGGAGTGTGTGTGCTCGGACACTCTCTGGGCAATCCCTGGGCTCCC 180

Qy 181 CTGAGCAGCTGCCCCAGCCAGGCGCTCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 240
Db 181 CTGAGCAGCTGCCCCAGCCAGGCGCTCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 240

Qy 241 GGCCTTTTCTCTACAGGGGCTCCCTGCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300
Db 241 GGCCTTTTCTCTACAGGGGCTCCCTGCCAGGCGCTTGAAGGATCTCCCGAGTTGGGT 300

Qy 301 CCCACCTTGAGACACTGAGCTGGAGCTGCCGACTTTGCCACCACTCTGGCAGCAG 360
Db 301 CCCACCTTGAGACACTGAGCTGGAGCTGCCGACTTTGCCACCACTCTGGCAGCAG 360

Qy 361 ATGGAAGAACTGGGAATGGCCCTGCTGCACGCCACCCAGGGTCCCATGCGGCTTTC 420
Db 361 ATGGAAGAACTGGGAATGGCCCTGCTGCACGCCACCCAGGGTCCCATGCGGCTTTC 420

Qy 421 GCCTCTGCTTTCCAGGCGCGGGCAGGAGGGTCTTAGTTGCTTCCCATCTGAGAGCTTC 480
Db 421 GCCTCTGCTTTCCAGGCGCGGGCAGGAGGGTCTTAGTTGCTTCCCATCTGAGAGCTTC 480

Qy	361	ATGGAGAACTGGGAATGGCCCTGCTGCGAGCCACCCAGGGTGCCATGCCGGCCTTC	420
Db	361	ATGGAGAACTGGGAATGGCCCTGCTGCGAGCCACCCAGGGTGCCATGCCGGCCTTC	420
Qy	421	GCCTCTGCTTTCCAGCGCGGGCGCAGGAGGGGTCTTAGTTGCTTCCCATCTGCAGAGCTTC	480
Db	421	GCCTCTGCTTTCCAGCGCGGGCGCAGGAGGGGTCTTAGTTGCTTCCCATCTGCAGAGCTTC	480
Qy	481	CTGGAGGTGTGCTACCGCGTTCTAGCCACCTTGCCAGCCCT	523
Db	481	CTGGAGGTGTGCTACCGCGTTCTAGCCACCTTGCCAGCCCT	523

Search completed: October 9, 2004, 06:22:17
 Job time : 452.349 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 01:28:34 ; Search time 80.3471 Seconds
(without alignments)
3612.319 Million cell updates/sec

Title: US-10-009-792C-18_COPY_88_610

Perfect score: 523

Sequence: 1 accccctggccctgcag.....acgccacttgccacgccct 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	523	100.0	525	1	US-08-434-411-1
2	523	100.0	525	1	US-08-434-402-1
3	523	100.0	525	1	US-08-783-288-1
4	523	100.0	525	2	US-08-890-640-1
5	523	100.0	525	6	5194592-25
6	510.2	97.6	541	2	US-08-797-689-13
7	510.2	97.6	541	4	US-09-984-186-13
8	510.2	97.6	2382	1	US-08-256-938-1
9	509.2	97.4	2455	1	US-08-256-938-3
10	509.2	97.4	2455	2	US-08-797-689-15
11	509.2	97.4	2455	4	US-08-984-186-15
12	507	96.9	525	3	US-08-149-101A-1
13	507	96.9	525	5	PCT-US94-12873-1
14	503.8	96.3	546	3	US-08-469-318-177
15	503.8	96.3	546	3	US-08-468-609A-177
16	503.8	96.3	546	4	US-08-446-872A-177
17	503.8	96.3	546	4	US-08-762-227A-177
18	503.8	96.3	546	5	PCT-US95-01185-177
19	503.8	96.3	921	3	US-08-469-318-72
20	503.8	96.3	921	3	US-08-469-318-75
21	503.8	96.3	921	3	US-08-469-318-78
22	503.8	96.3	921	3	US-08-468-609A-72
23	503.8	96.3	921	3	US-08-468-609A-75
24	503.8	96.3	921	3	US-08-468-609A-77
25	503.8	96.3	921	4	US-08-446-872A-72
26	503.8	96.3	921	4	US-08-446-872A-75
27	503.8	96.3	921	4	US-08-446-872A-78

28	503.8	96.3	921	4	US-08-762-227A-72
29	503.8	96.3	921	4	US-08-762-227A-75
30	503.8	96.3	921	4	US-08-762-227A-78
31	503.8	96.3	921	5	PCT-US95-01185-72
32	503.8	96.3	921	5	PCT-US95-01185-75
33	503.8	96.3	921	5	PCT-US95-01185-78
34	503.8	96.3	966	3	US-08-469-318-73
35	503.8	96.3	966	3	US-08-469-318-77
36	503.8	96.3	966	3	US-08-468-609A-73
37	503.8	96.3	966	3	US-08-468-609A-77
38	503.8	96.3	966	3	US-08-468-609A-79
39	503.8	96.3	966	4	US-08-446-872A-73
40	503.8	96.3	966	4	US-08-446-872A-77
41	503.8	96.3	966	4	US-08-446-872A-79
42	503.8	96.3	966	4	US-08-762-227A-73
43	503.8	96.3	966	4	US-08-762-227A-77
44	503.8	96.3	966	4	US-08-762-227A-79
45	503.8	96.3	966	4	US-08-762-227A-79

ALIGNMENTS

RESULT 1
US-08-434-411-1
Sequence 1, Application US/08434411
Patent No. 5681720
GENERAL INFORMATION:
APPLICANT: KUGA, TETSURO
APPLICANT: MIYAJI, HIROMASA
APPLICANT: SATO, MORIYUKI
APPLICANT: OKABE, MASAMI
APPLICANT: MORIMOTO, MAKOTO
APPLICANT: ITOH, SEIGA
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YOKOO, YOSHIHARU
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,411
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306799/86
FILING DATE: 23-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 80088/88
FILING DATE: 31-MAR-1988
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

```

;
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..522
; OTHER INFORMATION: /product= "HUMAN GRANULOCYTE COLONY
; OTHER INFORMATION: STIMULATING FACTOR"
;
US-08-434-411-1

Query Match 100.0%; Score 523; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 5.5e-115;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTCTAGAGCAA 60
DB 1 ACCCCCTGGGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTCTAGAGCAA 60
QY 61 GTGAGGAAGATCAGGGGATGGCGAGCGCTCCAGGAGAGCTGTGTCACCTTACAG 120
DB 61 GTGAGGAAGATCAGGGGATGGCGAGCGCTCCAGGAGAGCTGTGTCACCTTACAG 120
QY 121 CTGTGCCACCCGAGAGCTGTGCTGCTCGACACTCTCTGGGATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCGAGAGCTGTGCTGCTCGACACTCTCTGGGATCCCTGGGCTCCC 180
QY 181 CTGAGCAGCTGCCAGAGGCTGTGCTGCTCGAGCTGGAGGATCTGTCACCTTACAG 240
DB 181 CTGAGCAGCTGCCAGAGGCTGTGCTGCTCGAGCTGGAGGATCTGTCACCTTACAG 240
QY 241 GGCCTTTTCTTACCAAGGGCTTCTGCAAGGCCCTGGAAGGATCTCCCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTTACCAAGGGCTTCTGCAAGGCCCTGGAAGGATCTCCCCCGAGTTGGGT 300
QY 301 CCCACCTTGGACACTGAGCTGGACGTCGCGACTTTCGCCAGCTTTCGCCAGGCTTC 360
DB 301 CCCACCTTGGACACTGAGCTGGACGTCGCGACTTTCGCCAGGCTTTCGCCAGGCTTC 360
QY 361 ATGGAAGACTGGATGCCCCCTGCTGCGAGCCCTGCGAGGCTGCTGCGAGGCTTC 420
DB 361 ATGGAAGACTGGATGCCCCCTGCTGCGAGCCCTGCGAGGCTGCTGCGAGGCTTC 420
QY 421 GCTCTGCTTTCAGGCGCGGAGAGGGGCTCTAGTTGCTTCCCTTCCATCTGCAAGCTTC 480
DB 421 GCTCTGCTTTCAGGCGCGGAGAGGGGCTCTAGTTGCTTCCCTTCCATCTGCAAGCTTC 480
QY 481 CTGGAGGTGTGACCGCTTCTAGCCACCTTTCGCCAGGCTTC 523
DB 481 CTGGAGGTGTGACCGCTTCTAGCCACCTTTCGCCAGGCTTC 523

```

RESULT 2

```

US-08-434-402-1
; Sequence 1, Application US/08434402
; Patent No. 5714581
; GENERAL INFORMATION:
; APPLICANT: KUGA, TETSURO
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: SATO, MORIYUKI
; APPLICANT: OKABE, MASAMI
; APPLICANT: MORIMOTO, MAKOTO
; APPLICANT: ITOH, SEIGA
; APPLICANT: YAMASAKI, MOTOO
; APPLICANT: YOKOO, YOSHIMARU
; APPLICANT: YAMAGUCHI, KAZUO
; APPLICANT: YOSHIDA, HAJIME
; APPLICANT: YOSHINORI, KOMATSU
; TITLE OF INVENTION: NOVEL POLYPEPTIDES

```

```

;
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,402
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 306799/86
; FILING DATE: 23-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 51357/88
; FILING DATE: 04-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 80088/88
; FILING DATE: 31-MAR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR
; REGISTRATION NUMBER: 25327
; REFERENCE/DOCKET NUMBER: 249-72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..522
; OTHER INFORMATION: /product= "HUMAN GRANULOCYTE COLONY
; OTHER INFORMATION: STIMULATING FACTOR"
;
US-08-434-402-1

```

```

Query Match 100.0%; Score 523; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 5.5e-115;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTCTAGAGCAA 60
DB 1 ACCCCCTGGGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTCTAGAGCAA 60
QY 61 GTGAGGAAGATCAGGGGATGGCGAGCGCTCCAGGAGAGCTGTGTCACCTTACAG 120
DB 61 GTGAGGAAGATCAGGGGATGGCGAGCGCTCCAGGAGAGCTGTGTCACCTTACAG 120
QY 121 CTGTGCCACCCGAGAGCTGTGCTGCTCGACACTCTCTGGGATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCGAGAGCTGTGCTGCTCGACACTCTCTGGGATCCCTGGGCTCCC 180
QY 181 CTGAGCAGCTGCCAGAGGCTGTGCTGCTCGAGCTGGAGGATCTGTCACCTTACAG 240
DB 181 CTGAGCAGCTGCCAGAGGCTGTGCTGCTCGAGCTGGAGGATCTGTCACCTTACAG 240
QY 241 GGCCTTTTCTTACCAAGGGCTTCTGCAAGGCCCTGGAAGGATCTCCCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTTACCAAGGGCTTCTGCAAGGCCCTGGAAGGATCTCCCCCGAGTTGGGT 300
QY 301 CCCACCTTGGACACTGAGCTGGACGTCGCGACTTTCGCCAGCTTTCGCCAGGCTTC 360

```


STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,640
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/434,411
 FILING DATE: 03-MAY-1995
 APPLICATION NUMBER: JP 306799/86
 FILING DATE: 23-DEC-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 51357/88
 FILING DATE: 04-MAR-1988
 APPLICATION DATA:
 APPLICATION NUMBER: JP 80088/88
 FILING DATE: 31-MAR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAWFORD, ARTHUR
 REGISTRATION NUMBER: 25327
 REFERENCE/DOCKET NUMBER: 249-73
 TELEPHONE: (703)816-4000
 TELEFAX: (703)816-4100
 TELEX: 200797 NIXN UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 525 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..522
 OTHER INFORMATION: /product= "HUMAN GRANULOCYTE COLONY
 OTHER INFORMATION: STIMULATING FACTOR"
 US-08-890-640-1

Query Match 100.0%; Score 523; DB 2; Length 525;
 Best Local Similarity 100.0%; Pred. No. 5.5e-115; Mismatches 0; Indels 0; Gaps 0;
 Matches 523; Conservative 0;
 QY 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 60
 Db 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 60
 QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
 Db 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
 QY 121 CTGTGCCACCCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGCACTCTCTGGGCTCCC 180
 Db 121 CTGTGCCACCCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGCACTCTCTGGGCTCCC 180
 QY 181 CTGAGCAGCTGCCCGAGGCGCTTGCAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
 Db 181 CTGAGCAGCTGCCCGAGGCGCTTGCAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
 QY 241 GGCTTTTCTCTTACCAAGGGGCTCTGTGAGGCGCTTGAAGGGATCTCCCGGAGTTGGGT 300
 Db 241 GGCTTTTCTCTTACCAAGGGGCTCTGTGAGGCGCTTGAAGGGATCTCCCGGAGTTGGGT 300
 QY 301 CCACCTTTGACACACTGACGTGGACGTGGCGAGCTTTGCCACCACTCTGGCAGCAG 360
 Db 301 CCACCTTTGACACACTGACGTGGACGTGGCGAGCTTTGCCACCACTCTGGCAGCAG 360
 QY 361 ATGGAAGAACTGGGAATGGCCCTTGCCTGTCAGCCCACTCCAGGCTGCCATGCCGCTTC 420
 Db 361 ATGGAAGAACTGGGAATGGCCCTTGCCTGTCAGCCCACTCCAGGCTGCCATGCCGCTTC 420
 QY 421 GCCTCTGCTTTCCAGCGCGGGGAGGGGTCTAGTTGCTCCCTCCATCTGAGAGCTTC 480
 Db 421 GCCTCTGCTTTCCAGCGCGGGGAGGGGTCTAGTTGCTCCCTCCATCTGAGAGCTTC 480
 QY 481 CTGAGGTGTCTGACCGGCTTCTACGCCACCTTGGCCAGCCCT 523
 Db 481 CTGAGGTGTCTGACCGGCTTCTACGCCACCTTGGCCAGCCCT 523

RESULT 6

QY 361 ATGGAAGAACTGGGAATGGCCCTTGCCTGTCAGCCCACTCCAGGCTGCCATGCCGCTTC 420
 Db 361 ATGGAAGAACTGGGAATGGCCCTTGCCTGTCAGCCCACTCCAGGCTGCCATGCCGCTTC 420
 QY 421 GCCTCTGCTTTCCAGCGCGGGGAGGGGTCTAGTTGCTCCCTCCATCTGAGAGCTTC 480
 Db 421 GCCTCTGCTTTCCAGCGCGGGGAGGGGTCTAGTTGCTCCCTCCATCTGAGAGCTTC 480
 QY 481 CTGAGGTGTCTGACCGGCTTCTACGCCACCTTGGCCAGCCCT 523
 Db 481 CTGAGGTGTCTGACCGGCTTCTACGCCACCTTGGCCAGCCCT 523

RESULT 5
 5194592-25
 ; Patent No. 5194592
 ; APPLICANT: YOSHIDA, HAJIME
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
 ; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY
 ; STIMULATING FACTOR
 ; NUMBER OF SEQUENCES: 83
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/318,527
 ; FILING DATE: 3-MAR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 136,647
 ; FILING DATE: 22-DEC-1987
 ; SEQ ID NO: 25;
 ; LENGTH: 525
 5194592-25

Query Match 100.0%; Score 523; DB 6; Length 525;
 Best Local Similarity 100.0%; Pred. No. 5.5e-115;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 60
 Db 1 ACCCCCTGGGCTCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGTAGAGCAA 60
 QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
 Db 61 GTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
 QY 121 CTGTGCCACCCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGCACTCTCTGGGCTCCC 180
 Db 121 CTGTGCCACCCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGCACTCTCTGGGCTCCC 180
 QY 181 CTGAGCAGCTGCCCGAGGCGCTTGCAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
 Db 181 CTGAGCAGCTGCCCGAGGCGCTTGCAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
 QY 241 GGCTTTTCTCTTACCAAGGGGCTCTGTGAGGCGCTTGAAGGGATCTCCCGGAGTTGGGT 300
 Db 241 GGCTTTTCTCTTACCAAGGGGCTCTGTGAGGCGCTTGAAGGGATCTCCCGGAGTTGGGT 300
 QY 301 CCACCTTTGACACACTGACGTGGACGTGGCGAGCTTTGCCACCACTCTGGCAGCAG 360
 Db 301 CCACCTTTGACACACTGACGTGGACGTGGCGAGCTTTGCCACCACTCTGGCAGCAG 360
 QY 361 ATGGAAGAACTGGGAATGGCCCTTGCCTGTCAGCCCACTCCAGGCTGCCATGCCGCTTC 420
 Db 361 ATGGAAGAACTGGGAATGGCCCTTGCCTGTCAGCCCACTCCAGGCTGCCATGCCGCTTC 420
 QY 421 GCCTCTGCTTTCCAGCGCGGGGAGGGGTCTAGTTGCTCCCTCCATCTGAGAGCTTC 480
 Db 421 GCCTCTGCTTTCCAGCGCGGGGAGGGGTCTAGTTGCTCCCTCCATCTGAGAGCTTC 480
 QY 481 CTGAGGTGTCTGACCGGCTTCTACGCCACCTTGGCCAGCCCT 523
 Db 481 CTGAGGTGTCTGACCGGCTTCTACGCCACCTTGGCCAGCCCT 523

US-08-797-689-13
; Sequence 13, Application US/08797689
; Patent No. 5876369
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guittou, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..536
US-08-797-689-13

Query Match 97.6%; Score 510.2; DB 2; Length 541;
Best Local Similarity 98.5%; Pred. No. 5.9e-112;
Matches 515; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTGCGAGCTCCCTGCCCCAGAGCTTCTGCTCAAGTGCTTAGAGCAA 60
DB 12 ACCCCCTGGGCGCTGCGAGCTCCCTGCCCCAGAGCTTCTGCTCAAGTGCTTAGAGCAA 71
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGTGCCACTACAAG 120
DB 72 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGTGCCACTACAAG 131
QY 121 CTGTGCCACCCCGAGAGCTGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 132 CTGTGCCACCCCGAGAGCTGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 191
QY 181 CTGAGCAGTCCCCCAGCCAGGCCCTGCGAGTGGCAGGCTCTGAGCCAACTCCATAGC 240

Db 192 CTGAGCTCCTGCCCCAGCCAGCCCTGCGAGCTGGCAGGCTGTTGAGCCAACTCCATAGC 251
QY 241 GGCCTTTTCTCTACAGGGGCTCTGAGGCGCTTGGAGGGATCTCCCGAGTTGGGT 300
Db 252 GGCCTTTTCTCTACAGGGGCTCTGAGGCGCTTGGAGGGATCTCCCGAGTTGGGT 311
QY 301 CCCACCTTGGACACACTGCGAGCTGGACGCTGCGCGACTTTGCCACCACCATCTGGCAGCAG 360
Db 312 CCCACCTTGGACACACTGCGAGCTGGACGCTGCGCGACTTTGCCACCACCATCTGGCAGCAG 371
QY 361 ATGGAAGAAGCTGGGAATGCCCCCTGCGCTGCGAGCGCCAGCCAGGTTGCCATGCCGCGCTTC 420
Db 372 ATGGAAGAAGCTGGGAATGCCCCCTGCGCTGCGAGCGCCAGCCAGGTTGCCATGCCGCGCTTC 431
QY 421 GCCTCTGCTTTCCAGCGCGCGGAGGAGGCTCTAGTTGCTTCCCATCTGCAGAGCTTC 480
Db 432 GCCTCTGCTTTCCAGCGCGCGGAGGAGGCTCTAGTTGCTTCCCATCTGCAGAGCTTC 491
QY 481 CTGAGGCTGCTGACCGCTTCTACGCCACCTTGGCCAGCCCT 523
Db 492 CTGAGGCTGCTGACCGCTTCTACGCCACCTTGGCCAGCCCT 534

RESULT 7
US-09-984-186-13
; Sequence 13, Application US/09984186
; Patent No. 6686179
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guittou, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 base pairs

```

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..536
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-984-186-13

Query Match          97.6%; Score 510.2; DB 4; Length 541;
Best Local Similarity 98.5%; Pred. No. 5.9e-112;
Matches 515; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTCTTAGAGCAA 60
DB 12 ACCCCCTGGGCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTCTTAGAGCAA 71
QY 61 GTGAGGAAGATCCAGGGCAGTGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAA 120
DB 72 GTGAGGAAGATCCAGGGCAGTGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAA 131
QY 121 CTGTGTCACCCCGAGAGAGTGTGTGCTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 132 CTGTGTCACCCCGAGAGAGTGTGTGCTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 191
QY 181 CTGAGGAGTGTGCCAGCCAGGAGCTGTGCTGAGCTGGGAGAGCTGTGTGAGCAACTCCATAGC 240
DB 192 CTGAGCTCTGCCCCAGGAGGCTGTGCTGAGCTGGGAGAGCTGTGTGAGCAACTCCATAGC 251
QY 241 GGCCTTTTCTCTACCAAGGGCTCTGAGGAGGCTGTGAGGAGGATCTCCCGAGTTGGGT 300
DB 252 GGCCTTTTCTCTACCAAGGGCTCTGAGGAGGCTGTGAGGAGGATCTCCCGAGTTGGGT 311
QY 301 CCACCTTGGACACACTGAGCTGAGCTGCGCGACTTTTGGCCACCACTCTGGAGCAG 360
DB 312 CCACCTTGGACACACTGAGCTGAGCTGCGCGACTTTTGGCCACCACTCTGGAGCAG 371
QY 361 ATGGAAGAACTGGGAATGCGCCCTGCTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTTC 420
DB 372 ATGGAAGAACTGGGAATGCGCCCTGCTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTTC 431
QY 421 GCCTCTGCTTCCAGCGCGGAGAGAGGGGCTCTAGTGTGCTCCATCTGAGAGCTTC 480
DB 432 GCCTCTGCTTCCAGCGCGGAGAGAGGGGCTCTAGTGTGCTCCATCTGAGAGCTTC 491
QY 481 CTGGAGGTGTCTACCGGCTTCTAGCCACCTTGGCCAGCCCT 523
DB 492 CTGGAGGTGTCTACCGGCTTCTAGCCACCTTGGCCAGCCCT 534

RESULT 8
US-08-256-938-1
; Sequence 1, Application US/08256938
; Patent No. 565863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)

```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: FR 92/01065
; APPLICATION NUMBER:
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2382 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 26..2377
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1842..1848
; OTHER INFORMATION: /label= MstII-site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1861..1866
; OTHER INFORMATION: /label= ApaI-site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2035..2040
; OTHER INFORMATION: /label= SstI-site
; US-08-256-938-1

Query Match          97.6%; Score 510.2; DB 1; Length 2382;
Best Local Similarity 98.5%; Pred. No. 8.2e-112;
Matches 515; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTCTTAGAGCAA 60
DB 1853 ACCCCCTGGGCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTCTTAGAGCAA 1912
QY 61 GTGAGGAAGATCCAGGGCAGTGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAA 120
DB 1913 GTGAGGAAGATCCAGGGCAGTGGCGAGGCTCCAGGAGAGCTGTGTGCCACCTACAA 1972
QY 121 CTGTGTCACCCCGAGGAGTGTGTGCTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 1973 CTGTGTCACCCCGAGGAGTGTGTGCTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 2032
QY 181 CTGAGCAGCTGCCCGCAGCCAGGCTTCGAGCTGGGAGGCTGTGTGAGCAACTCCATAGC 240
DB 2033 CTGAGCTCTGCCCCAGCCAGGCTTCGAGCTGGGAGGCTGTGTGAGCAACTCCATAGC 2092
QY 241 GGCCTTTTCTCTACCAAGGGCTCTCTGAGGAGGCTTCGAAAGGATATCCCGAGTTGGGT 300
DB 2093 GGCCTTTTCTCTACCAAGGGCTCTCTGAGGAGGCTTCGAAAGGATATCCCGAGTTGGGT 2152
QY 301 CCACCTTGGACACACTGAGCTGTGAGCTGTGCGGACTTTTGGCCACCACTCTGGAGCAG 360
DB 2153 CCACCTTGGACACACTGAGCTGTGAGCTGTGCGGACTTTTGGCCACCACTCTGGAGCAG 2212
QY 361 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCACCCAGGCTGCCATGCCGGCTTC 420
DB 2213 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCACCCAGGCTGCCATGCCGGCTTC 2272
QY 421 GCCTCTGCTTTCAGCGCGGAGAGGGGCTCTAGTGTGCTCCATCTGAGAGCTTC 480

```

Db 2273 GCCTCTGCTTCCAGCGCCGCGAGGAGGGTCTCTGTTGCTAGCCATCTGCAGAGCTTC 2332
QY 481 CTGGAGGTGTCGTACCGGTTCTACGCCACCTTGCAGCCCT 523
Db 2333 CTGGAGGTGTCGTACCGGTTCTACGCCACCTTGGCAGCCCT 2375

RESULT 9
US-08-256-938-3
; Sequence 3, Application US/08256938
; Patent No. 5655863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 26..2389
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 106..111
; OTHER INFORMATION: /label= Apai-site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 280..285
; OTHER INFORMATION: /label= Ssti-site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2376..2382
; OTHER INFORMATION: /label= MstII-site
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 26..97
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: 620..631
; OTHER INFORMATION: /label= polygly-linker
US-08-256-938-3
Query Match 97.4%; Score 509.2; DB 1; Length 2455;
Best Local Similarity 98.5%; Pred. No. 1.4e-111;
Matches 514; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ACCCCCTGGCCCTGCGAGCTCCCTGCCAGAGCTTCTGCTCCAGTCTTAGAGCAA 60
Db 98 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCCAGTCTTAGAGCAA 157
QY 61 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAAAGCTGTGTGCCACCTACAG 120
Db 158 GTGAGGAAGATCCAGGGCGATGCGCAGCGCTCCAGGAAAGCTGTGTGCCACCTACAG 217
QY 121 CTGTGCCACCCCGAGGAGCTGTGTCTCGACACTCTCTCGGCATCCCTGGGCTCC 180
Db 218 CTGTGCCACCCCGAGGAGCTGTGTCTCGACACTCTCTCGGCATCCCTGGGCTCC 277
QY 181 CTGAGCAGCTGCCCGCAGCCAGCCCTGCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
Db 278 CTGAGCTCTGCCCGCAGCCAGCCCTGCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 337
QY 241 GGCCTTTTCTCTTACCAGGGGCTCTGCGAGGCGCTGGAAGGATCTCCCCCGAGTTGGGT 300
Db 338 GGCCTTTTCTCTTACCAGGGGCTCTGCGAGGCGCTGGAAGGATCTCCCCCGAGTTGGGT 397
QY 301 CCCACCTTGGACACACTGAGCTGAGCTGCGGAGCTTTGCCACACCACTCTGGCAGCAG 360
Db 398 CCCACCTTGGACACACTGAGCTGAGCTGCGGAGCTTTGCCACACCACTCTGGCAGCAG 457
QY 361 ATGGAAGAACTGGGAATGCCCTGCCTCGAGCCAGCCACCCAGGCTGCCATGCCGGCTTC 420
Db 458 ATGGAAGAACTGGGAATGCCCTGCCTCGAGCCAGCCACCCAGGCTGCCATGCCGGCTTC 517
QY 421 GCCTCTGCTTTCAGCGCCGGGAGAGGGGTCCTAGTTCCTCCCATCTGCAGAGCTTC 480
Db 518 GCCTCTGCTTTCAGCGCCGGGAGAGGGGTCCTAGTTCCTCCCATCTGCAGAGCTTC 577
QY 481 CTGGAGGTGCTGACCGGCTTCTAGCCACCTTGCCAGCCC 522
Db 578 CTGGAGGTGCTGACCGGCTTCTAGCCACCTTGCCAGCCC 619
RESULT 10
US-08-797-689-15
; Sequence 15, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guitten, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689

```

; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 26..2389
; US-08-797-689-15

Query Match          97.4%; Score 509.2; DB 2; Length 2455;
Best Local Similarity 98.5%; Pred. No. 1.4e-111;
Matches 514; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTAGAGCAA 60
Db 98 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTAGAGCAA 157
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGCGACCTACAG 120
Db 158 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGCGACCTACAG 217
QY 121 CTGTGACACCCCGAGGAGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 180
Db 218 CTGTGACACCCCGAGGAGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 277
QY 181 CTGAGAGCTGCCCCAGCAGGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 240
Db 278 CTGAGCTCTGCCCCAGCAGGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 337
QY 241 GGCCTTTTCTCTTACAGGGGCTCTGAGGGGCTTGAAGGATCTCCCGAGTTGGGT 300
Db 338 GGCCTTTTCTCTTACAGGGGCTCTGAGGGGCTTGAAGGATCTCCCGAGTTGGGT 397
QY 301 CCCACCTTGGACACACTGAGTGGAGCTGCGCGACTTTGCGACCACTTGGCAGCAG 360
Db 398 CCCACCTTGGACACACTGAGTGGAGCTGCGCGACTTTGCGACCACTTGGCAGCAG 457
QY 361 ATGGAGAGTGGGATGCCCTGCTGCGAGCCCAACCCAGGGTGCATGCCGCTTC 420
Db 458 ATGGAGAGTGGGATGCCCTGCTGCGAGCCCAACCCAGGGTGCATGCCGCTTC 517
QY 421 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTTAGTTGCTTCCCATCTGCGAGCTTC 480
Db 518 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTTAGTTGCTTCCCATCTGCGAGCTTC 577
QY 481 CTGGAGGTGTGTTACCGGCTTCTAGCCACCTTGGCCAGCCC 522
Db 578 CTGGAGGTGTGTTACCGGCTTCTAGCCACCTTGGCCAGCCC 619

RESULT 11
US-09-984-186-15
; Sequence 15, Application US/09984186

; Patent No. 6686179
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-OCT-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 26..2389
; US-09-984-186-15

Query Match          97.4%; Score 509.2; DB 4; Length 2455;
Best Local Similarity 98.5%; Pred. No. 1.4e-111;
Matches 514; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTAGAGCAA 60
Db 98 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTAGAGCAA 157
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGCGACCTACAG 120
Db 158 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGCGACCTACAG 217
QY 121 CTGTGACACCCCGAGGAGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 180
Db 218 CTGTGACACCCCGAGGAGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 277
QY 181 CTGAGAGCTGCCCCAGCAGGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 240
Db 278 CTGAGCTCTGCCCCAGCAGGCTGTGCTGCGACACTCTCTGGGATCCCTGGGCTCCC 337
QY 241 GGCCTTTTCTCTTACAGGGGCTCTGAGGGGCTTGAAGGATCTCCCGAGTTGGGT 300
Db 338 GGCCTTTTCTCTTACAGGGGCTCTGAGGGGCTTGAAGGATCTCCCGAGTTGGGT 397
QY 301 CCCACCTTGGACACACTGAGTGGAGCTGCGCGACTTTGCGACCACTTGGCAGCAG 360
Db 398 CCCACCTTGGACACACTGAGTGGAGCTGCGCGACTTTGCGACCACTTGGCAGCAG 457
QY 361 ATGGAGAGTGGGATGCCCTGCTGCGAGCCCAACCCAGGGTGCATGCCGCTTC 420
Db 458 ATGGAGAGTGGGATGCCCTGCTGCGAGCCCAACCCAGGGTGCATGCCGCTTC 517
QY 421 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTTAGTTGCTTCCCATCTGCGAGCTTC 480
Db 518 GCCTCTGCTTTCAGCGCGGGCAGAGGGGTCTTAGTTGCTTCCCATCTGCGAGCTTC 577
QY 481 CTGGAGGTGTGTTACCGGCTTCTAGCCACCTTGGCCAGCCC 522
Db 578 CTGGAGGTGTGTTACCGGCTTCTAGCCACCTTGGCCAGCCC 619

RESULT 11
US-09-984-186-15
; Sequence 15, Application US/09984186
```


[illegible]

RESULT 12

US-08-149-101A-1
; Sequence 1, Application US/08149101A

```

; Patent No. 6171824
;
; GENERAL INFORMATION:
;
; APPLICANT: Todaro, George J.
; APPLICANT: Leung, David W.
; APPLICANT: Rose, Timothy M.
;
; TITLE OF INVENTION: HYBRID CYTOKINES
;
; NUMBER OF SEQUENCES: 26
;
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Cell Inerapeutics, Inc.
STREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" disk, 1.44Mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,101A
FILING DATE: 8-No. 6171824-1993

;	INDIVIDUAL ISOLATE:
;	DEVELOPMENTAL STAGE:
;	HAPLOTYPE:
;	TISSUE TYPE:
;	CELL TYPE:
;	CELL LINE:
;	ORGANELLE:
;	IMMEDIATE SOURCE:
;	LIBRARY: Fred Hutchinson Cancer Research Center
;	CLONE:
;	POSITION IN GENOME:
;	CHROMOSOME/SEGMENT:
;	MAP POSITION:
;	UNITS:
;	FEATURE:
;	NAME/KEY: G-CSF
;	LOCATION:
;	IDENTIFICATION METHOD:
;	OTHER INFORMATION:
;	PUBLICATION INFORMATION:
;	AUTHORS:
;	TITLE:
;	JOURNAL:
;	VOLUME:
;	ISSUE:
;	PAGES:
;	DATE:
;	DOCUMENT NUMBER:
;	FILING DATE:
;	PUBLICATION DATE:
;	RELEVANT RESIDUES IN SEQ ID NO: 1:
;	US-08-149-101A-1
	Query Match 96.9%; Score 507; DB 3; Length 525;
	Best Local Similarity 98.1%; Pred. No. 3.3e-111;
	Matches 513; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy	1 ACCCCCCTGGCCCTGCCAGCTCCCTGCCCGACGCTTCGTCTCAAGTCTTGAGCAA 60
Dd	1 ACCCCCCTGGCCCTGCCAGCTCCCTGCCCGACGCTTCGTCTCAAGTCTTGAGCAA 60
Qy	61 GTGAGAAGATCCAGGSCGATGGCGCAGCGCTCCAGAGAAGCTGTGTGCCACTACAAG 120
Dd	61 GTGAGAAGATCCAGGSCGATGGCGCAGCGCTCCAGAGAAGCTGTGTGCCACTACAAG 120
Qy	121 CTGTGCCACCCGAGAGCTGTGTCTGTCTGGACACTCTCTGGGCATCCCTGGGCTCCC 180
Dd	121 CTGTGCCACCCGAGAGCTGTGTCTGTCTGGACACTCTCTGGGCATCCCTGGGCTCCC 180
Qy	181 CTGAGCAGCTGCCCCCAGCCAGGCGCTGCAGCTGGCAGGCTGTGAGCCAACTCCATAGC 240
Dd	181 CTGAGCAGCTGCCCCCAGCCAGGCGCTGCAGCTGGCAGGCTGTGAGCCAACTCCATAGC 240
Qy	241 GGCCTTTCTCTACGAGGGGCTCTGTGAGGCGCTGGGAAGGATCTCCCGGAGTTGGGT 300
Dd	241 GGCCTTTCTCTACGAGGGGCTCTGTGAGGCGCTGGGAAGGATCTCCCGGAGTTGGGT 300
Qy	301 CCCACCTTGACACACTGCAGCTGGAGCTGCCGACTTTGCCACCACCATCTGCAGCAG 360
Dd	301 CCCACCTTGACACACTGCAGCTGGAGCTGCCGACTTTGCCACCACCATCTGCAGCAG 360
Qy	361 ATGGAAGAACTGGGAATGGCCCTTGCCCTGCAGCCACCCAGGGTGCACTGCCGCTTC 420
Dd	361 ATGGAAGAACTGGGAATGGCCCTTGCCCTGCAGCCACCCAGGGTGCACTGCCGCTTC 420
Qy	421 GCCTCTCTTTTCAGCCCGGGGAGGAGGTCCTAGTTGCTCTCCCATCTGCAGAGTTC 480
Dd	421 GCCTCTCTTTTCAGCCCGGGGAGGAGGTCCTAGTTGCTCTCCCATCTGCAGAGTTC 480
Qy	481 CTGAGGTGTGCTAACCGCGTTCTACGCCACCTTGCCCGAGCCCT 523
Dd	481 CTGAGGTGTGCTAACCGCGTTCTACGCCACCTTGCCCGAGCCCT 523

RESULT 13

PCT-US94-12873-1
; Sequence 1, Application PC/TUS9412873
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 26
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12873
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; PCT-US94-12873-1

Query Match 96.9%; Score 507; DB 5; Length 525;
Best Local Similarity 98.1%; Pred. No. 3.3e-111; Indels 0; Gaps 0;
Matches 513; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ACCCCCCTGGCCCTGCCAGCTCCCTGCCCGAGCTTCTCTCAAGTGTAGAGCAA 60
Db 1 ACCCCCCTGGCCCTGCCAGCTCCCTGCCCGAGCTTCTCTCAAGTGTAGAGCAA 60
QY 61 GTGAGGAAGATCCAGGGCATGGCGAGCTCCAGGAGAGCTGTGCCACTTACAA 120
Db 61 GTGAGGAAGATCCAGGGCATGGCGAGCTCCAGGAGAGCTGTGCCACTTACAA 120
QY 121 CTGTGCGACCCCGAGAGCTGTGTCTCGACACTCTCTGGGCGATCCCTGGGCTCCC 180
Db 121 CTGTGCGACCCCGAGAGCTGTGTCTCGACACTCTCTGGGCGATCCCTGGGCTCCC 180
QY 181 CTGAGAGCTGCCCGAGAGCTGTGTCTCGACACTCTCTGGGCGATCCCTGGGCTCCC 240
Db 181 CTGAGAGCTGCCCGAGAGCTGTGTCTCGACACTCTCTGGGCGATCCCTGGGCTCCC 240
QY 241 GGCCCTTTCTCTACCGAGGGCTCTCTGAGGGCTTGGAGGGATCTCCCGAGTTGGGT 300
Db 241 GGCCCTTTCTCTACCGAGGGCTCTCTGAGGGCTTGGAGGGATCTCCCGAGTTGGGT 300
QY 301 CCACCTTGGACACACTGAGCTGAGCTGCGCGACTTGTGCCACCACTCTGGCAGCAG 360
Db 301 CCACCTTGGACACACTGAGCTGAGCTGCGCGACTTGTGCCACCACTCTGGCAGCAG 360
QY 361 ATGGAGAACTGGGAATGSCCTCTGCGAGCCCGAGGGTGCATGCCGCTTC 420
Db 361 ATGGAGAACTGGGAATGSCCTCTGCGAGCCCGAGGGTGCATGCCGCTTC 420
QY 421 GCCTCTGCTTTCAGCGCGGAGAGGGGTCTTAGTTGCTCCCATCTCGAGAGCTTC 480
Db 421 GCCTCTGCTTTCAGCGCGGAGAGGGGTCTTAGTTGCTCCCATCTCGAGAGCTTC 480
QY 481 CTGGAGGTGTCTGACCGGCTTCTAGCCACTTTCGCCAGCCCT 523
Db 481 CTGGAGGTGTCTGACCGGCTTCTAGCCACTTTCGCCAGCCCT 523

RESULT 14

US-08-469-318-177
; Sequence 177, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:

; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 177:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-469-318-177

Query Match 96.3%; Score 503.8; DB 3; Length 546;
Best Local Similarity 97.7%; Pred. No. 1.9e-110;
Matches 511; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ACCCCCCTGGCCCTGCCAGCTCCCTGCCCGAGCTTCTCTCAAGTGTAGAGCAA 60
Db 7 ACACCATTAGCCCTGCCAGCTCCCTGCCCGAGCTTCTCTCAAGTGTAGAGCAA 66
QY 61 GTGAGGAAGATCCAGGGCATGGCGAGCTCCAGGAGAGCTGTGCCACTTACAA 120
Db 67 GTGAGGAAGATCCAGGGCATGGCGAGCTCCAGGAGAGCTGTGCCACTTACAA 126
QY 121 CTGTGCGACCCCGAGAGCTGTGTCTCGGACACTCTCTGGGCGATCCCTGGGCTCCC 180
Db 127 CTGTGCGACCCCGAGAGCTGTGTCTCGGACACTCTCTGGGCGATCCCTGGGCTCCC 186
QY 181 CTGAGAGCTGCCCGAGAGCTGTGTCTCGGACACTCTCTGGGCGATCCCTGGGCTCCC 240
Db 187 CTGAGCTCTGCCCGAGAGCTGTGTCTCGGAGCTGTGTGAGCCAACTCCATAGC 246
QY 241 GGCCCTTTCTCTACCGAGGGCTCTCTGAGGGCTTGGAGGGATCTCCCGAGTTGGGT 300
Db 247 GGCCCTTTCTCTACCGAGGGCTCTCTGAGGGCTTGGAGGGATCTCCCGAGTTGGGT 306
QY 301 CCACCTTGGACACACTGAGCTGAGCTGCGCGACTTGTGCCACCACTCTGGCAGCAG 360
Db 307 CCACCTTGGACACACTGAGCTGAGCTGCGCGACTTGTGCCACCACTCTGGCAGCAG 366
QY 361 ATGGAGAACTGGGAATGSCCTCTGCGAGCCCGAGGGTGCATGCCGCTTC 420
Db 367 ATGGAGAACTGGGAATGSCCTCTGCGAGCCCGAGGGTGCATGCCGCTTC 426
QY 421 GCCTCTGCTTTCAGCGCGGAGAGGGGTCTTAGTTGCTCCCATCTCGAGAGCTTC 480
Db 427 GCCTCTGCTTTCAGCGCGGAGAGGGGTCTTAGTTGCTCCCATCTCGAGAGCTTC 486
QY 481 CTGGAGGTGTCTGACCGGCTTCTAGCCACTTTCGCCAGCCCT 523
Db 487 CTGGAGGTGTCTGACCGGCTTCTAGCCACTTTCGCCAGCCCT 529

RESULT 15

US-08-468-609A-177
; Sequence 177, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.

APPLICANT: Caparon, Mair H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-3)
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-609A-177

Query Match 96.3%; Score 503.8; DB 3; Length 546;
Best Local Similarity 97.7%; Pred No. 1.9e-110;
Matches 511; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
DB 7 ACACCAATTAGGCGCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 66
QY 61 GTGAGGAGATCCAGGGGATGGCGGAGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
DB 67 GTGAGGAGATCCAGGGGATGGCGGAGCTCCAGGAGAGCTGTGTGCCACCTACAAG 126
QY 121 CTGTGCCACCCCGAGGAGCTGTGTGTCTCGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB 127 CTGTGCCACCCCGAGGAGCTGTGTGTCTCGACACTCTCTGGGCATCCCTGGGCTCCC 186
QY 181 CTGAGCAGCTGCCCGAGGAGCTGTGTGTCTCGACACTCTCTGGGCATCCCTGGGCTCCC 240
DB 187 CTGAGCAGCTGCCCGAGGAGCTGTGTGTCTCGACACTCTCTGGGCATCCCTGGGCTCCC 246
QY 241 GGCCTTTTCTTACAGGGGCTCTCGAGGGCTTGAAGGATCTCCCGGAGTTGGGT 300
DB 247 GGCCTTTTCTTACAGGGGCTCTCGAGGGCTTGAAGGATATCCCGGAGTTGGGT 306
QY 301 CCCACCTTGGACACACTGAGCTGAGCTGTGTGTCTCGACACTCTCTGGGCATCCCTGGGCTCCC 360
DB 307 CCCACCTTGGACACACTGAGCTGAGCTGTGTGTCTCGACACTCTCTGGGCATCCCTGGGCTCCC 366

QY 361 ATGGAGAACTGGGAATGGCCCTGCTGAGAGCCACCCAGGTGCCATGCCGCTTC 420
DB 367 ATGGAGAACTGGGAATGGCCCTGCTGAGAGCCACCCAGGTGCCATGCCGCTTC 426
QY 421 GCTCTGCTTTCCAGCCCGGGCAGAGGGGTCTCTAGTTGCCATCTGCAGAGCTTC 480
DB 427 GCTCTGCTTTCCAGCCCGGGCAGAGGGGTCTCTAGTTGCCATCTGCAGAGCTTC 486
QY 481 CTGGAGGTGTCTGACCGGCTTCTAGCCACCTTGGCCAGCCCT 523
DB 487 CTGGAGGTGTCTGACCGGCTTCTAGCCACCTTGGCCAGCCCT 529

Search completed: October 9, 2004, 04:24:23
Job time : 83.3471 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 21:19:03 ; Search time 397.272 Seconds
(without alignments)
5592.665 Million cell updates/sec

Title: US-10-009-792C-18_COPY_88_610

Perfect score: 523

Sequence: 1 accccctggccctgacag.....acgccacctgcccagccct 523

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 337863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	100.0	525	1	Aan80947 G-CSF gen
2	523	100.0	531	4	Aad19772 Human hG-
3	523	100.0	615	4	Aad19771 Human hG-
4	523	100.0	1520	1	Aan70223 Plasmid p
5	523	100.0	1520	1	Aan71320 Sequence
6	523	100.0	1521	1	Aan60937 Plasmid p
7	523	100.0	1525	1	Aan81478 Sequence
8	523	100.0	1525	1	Aan91086 Plasmid p
9	521.4	99.7	525	7	Ac78869 Human gra
10	521.4	99.7	549	3	Aba94177 Granulocyte
11	521.4	99.7	1415	1	Aan71089 Sequence
12	521.4	99.7	1508	7	Abx63825 Human CDN
13	513.4	98.2	644	5	Aai17848 Recombina
14	510.2	97.6	540	2	Aaz21169 Recombina
15	510.2	97.6	556	1	Aan90533 Synthetic
16	510.2	97.6	777	3	Aaa71317 Mammalian
17	510.2	97.6	780	3	Aaa71312 MF alpha
18	510.2	97.6	2382	2	AaQ45987 Prepro-HS
19	509.2	97.4	2455	2	AaQ45988 G-CSF-(GL
20	508.6	97.2	1039	2	AaQ24283 IL-3-G-CS
21	507.6	97.1	522	4	Aaf56684 Human gra
22	507.6	96.9	525	2	AaQ87151 Human gra
23	506	96.7	522	6	ABK68973 CDNA enco

ALIGNMENTS

RESULT 1

AAN80947

ID AAN80947 standard; DNA; 525 BP.

XX AC

XX AAN80947;

XX DT 15-NOV-1990 (first entry)

XX XX

XX G-CSF gene isolated from peripheral blood macrophages.

XX DE Granulocyte colony stimulating factor; hg-CSF; macrophage;

XX KW tumour therapy; leukaemia; ss.

XX OS Homo sapiens.

XX XX

XX PN EP272703-A.

XX XX

XX PD 29-JUN-1988.

XX XX

XX PF 23-DEC-1987; 87EP-00119157.

XX XX

XX PR 23-DEC-1986; 86JP-00306799.

XX XX

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX XX

XX PI Kuga T, Komatsu Y, Miyaji H, Sato M, Okabe M, Morimoto M;

XX PI Itoh S, Yamasaki M;

XX XX

XX DR WPI; 1988-176825/26.

XX DR P-PSDB; AAP80965.

XX XX

XX PT Human granulocyte colony stimulating factor polypeptide derivs. - having

XX PT at least one different aminoacid, giving high specific activity and

XX PT stability.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

```
Query Match 100.0%; Score 523; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.2e-107;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
DB 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGTGCCACTTACAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGGCGAGCTTCAGGAGAGCTGTGTGCCACTTACAAG 120
QY 121 CTGTGTCACCCGAGAGTGTGTGTCTGTGCGACACTCTCTGGGCACTCCCTGGGCTCCC 180
DB 121 CTGTGTCACCCGAGAGTGTGTGTCTGTGCGACACTCTCTGGGCACTCCCTGGGCTCCC 180
QY 181 CTGAGCAGTGTCCCGAGCGCCCTGCAGCTGGCAGCTGCTTGAGCAACTCCATAGC 240
DB 181 CTGAGCAGTGTCCCGAGCGCCCTGCAGCTGGCAGCTGCTTGAGCAACTCCATAGC 240
QY 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCGCTTGAAGGATCTCCCGAGTGGGT 300
DB 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCGCTTGAAGGATCTCCCGAGTGGGT 300
QY 301 CCCACTTGGACACACTGCAGCTGCAGCTGCCGACTTGGCACCACCATCTGCAGCAG 360
DB 301 CCCACTTGGACACACTGCAGCTGCAGCTGCCGACTTGGCACCACCATCTGCAGCAG 360
QY 361 ATGGAAGAACTGGGAATGGCCCTCTGAGCGCCACCCAGGGTGCATGCCGGCTTC 420
DB 361 ATGGAAGAACTGGGAATGGCCCTCTGAGCGCCACCCAGGGTGCATGCCGGCTTC 420
QY 421 GCCTCTGCTTTCAGGGCGGAGAGGGTCTAGTGTGCTTCCATCTGCAGAGCTTC 480
DB 421 GCCTCTGCTTTCAGGGCGGAGAGGGTCTAGTGTGCTTCCATCTGCAGAGCTTC 480
QY 481 CTGGAGGTGTCTACCGGCTTCTACGCCACCTTGGCCAGCCCT 523
DB 481 CTGGAGGTGTCTACCGGCTTCTACGCCACCTTGGCCAGCCCT 523

RESULT 2
AAD19771
ID AAD19772 standard; DNA; 531 BP.
AC AAD19772;
XX
DT 18-DEC-2001 (first entry)
DE Human hG-CSF gene inserted into plasmid pEDCSFm.
KW Human; granulocyte colony stimulating factor; hG-CSF; protease;
XX Factor Xa; kanamycin resistance; endoxylanase signal peptide; ds.
OS Homo sapiens.
FH Key
FT CDS
FT /tag= a
FT /product= "Human hG-CSF protein"
XX
PN WO200173081-A1.
XX
PD 04-OCT-2001.
XX
PF 31-MAR-2001; 2001WO-KR000549.
XX
PR 31-MAR-2000; 2000KR-00017052.
XX
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
XX
PI Lee S, Jeong K;
```

```
XX WPI; 2001-616523/71.
DR P-PSDB; AAE12154.
XX
PT Recombinant plasmid vector comprising an endoxylanase signal sequence,
PT human granulocyte colony stimulating factor gene and other components,
PT when transformed into microorganism useful for preparing the colony
PT stimulating factor.
XX
PS Example 2; Fig 5; 50pp; English.
XX
CC The invention relates to an Escherichia coli producing and secreting
CC human granulocyte colony stimulating factor (hG-CSF), more specifically,
CC to a recombinant plasmid constructed to express secretory hG-CSF in E.
CC coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a
CC process for preparing hG-CSF using the transformed hG-CSF. The
CC recombinant plasmid vector comprises of a kanamycin resistance gene, a
CC promoter, an endoxylanase signal sequence, a nucleotide sequence coding
CC for an oligopeptide consisting of 13 amino acids including 6 consecutive
CC histidine residues and a hG-CSF. E.coli transformed with recombinant
CC plasmid vector is useful for preparing hG-CSF. The method comprises
CC culturing the microorganism to obtain a hG-CSF fusion protein and
CC treating the fusion protein with a protease preferably Factor Xa, to
CC obtain a hG-CSF, where the fusion protein is obtained from the culture by
CC employing Ni-column. The present sequence is human hG-CSF gene inserted
CC into plasmid pEDCSFm
XX
SQ Sequence 531 BP; 89 A; 192 C; 151 G; 99 T; 0 U; 0 Other;
```

```
Query Match 100.0%; Score 523; DB 4; Length 531;
Best Local Similarity 100.0%; Pred. No. 2.2e-107;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
DB 4 ACCCCCTGGGCGCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 63
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCTCCAGGAGAGCTGTGTGCCACTTACAAG 120
DB 64 GTGAGGAAGATCCAGGGCGATGGCGAGCTTCAGGAGAGCTGTGTGCCACTTACAAG 123
QY 121 CTGTGTCACCCGAGAGTGTGTGTCTGTGCGACACTCTCTGGGCACTCCCTGGGCTCCC 180
DB 124 CTGTGTCACCCGAGAGTGTGTGTCTGTGCGACACTCTCTGGGCACTCCCTGGGCTCCC 183
QY 181 CTGAGCAGTGTCCCGAGCGCCCTGCAGCTGGCAGCTGCTTGAGCAACTCCATAGC 240
DB 184 CTGAGCAGTGTCCCGAGCGCCCTGCAGCTGGCAGCTGCTTGAGCAACTCCATAGC 243
QY 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCGCTTGAAGGATCTCCCGAGTGGGT 300
DB 244 GGCCTTTTCTCTACAGGGGTCTCTGAGGCGCTTGAAGGATCTCCCGAGTGGGT 303
QY 301 CCCACTTGGACACACTGCAGCTGCAGCTGCCGACTTGGCACCACCATCTGCAGCAG 360
DB 304 CCCACTTGGACACACTGCAGCTGCAGCTGCCGACTTGGCACCACCATCTGCAGCAG 363
QY 361 ATGGAAGAACTGGGAATGGCCCTCTGAGCGCCACCCAGGGTGCATGCCGGCTTC 420
DB 364 ATGGAAGAACTGGGAATGGCCCTCTGAGCGCCACCCAGGGTGCATGCCGGCTTC 423
QY 421 GCCTCTGCTTTCAGGGCGGAGAGGGTCTAGTGTGCTTCCATCTGCAGAGCTTC 480
DB 424 GCCTCTGCTTTCAGGGCGGAGAGGGTCTAGTGTGCTTCCATCTGCAGAGCTTC 483
QY 481 CTGGAGGTGTCTACCGGCTTCTACGCCACCTTGGCCAGCCCT 523
DB 484 CTGGAGGTGTCTACCGGCTTCTACGCCACCTTGGCCAGCCCT 526
```

```
RESULT 3
AAD19771
ID AAD19771 standard; DNA; 615 BP.
```

```

XX AD19771;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human hG-CSF gene inserted into plasmid p19CSFm.
XX
XX Human; granulocyte colony stimulating factor; hG-CSF; protease;
XX Factor Xa; kanamycin resistance; endoxylanase signal peptide; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 88..612
XX /tag= a
XX /product= "Human hG-CSF protein"
XX /note= "CDS does not include start codon"
XX /partial
XX
XX WO200173081-A1.
XX
XX 04-OCT-2001.
XX
XX 31-MAR-2001; 2001WO-KR000549.
XX
XX 31-MAR-2000; 2000KR-00017052.
XX
XX (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
XX
XX Lee S, Jeong K;
XX
XX WPI; 2001-616523/71.
XX P-PSDB; AAE12153.
XX
XX Recombinant plasmid vector comprising an endoxylanase signal sequence,
XX human granulocyte colony stimulating factor gene and other components,
XX when transformed into microorganism useful for preparing the colony
XX stimulating factor.
XX
XX Example 1; Fig 3; 50pp; English.
XX
XX The invention relates to an Escherichia coli producing and secreting
XX human granulocyte colony stimulating factor (hG-CSF), more specifically,
XX to a recombinant plasmid constructed to express secretory hG-CSF in E.
XX coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a
XX process for preparing hG-CSF using the transformed hG-CSF. The
XX recombinant plasmid vector comprises of a kanamycin resistance gene, a
XX promoter, an endoxylanase signal sequence, a nucleotide sequence coding
XX for an oligopeptide consisting of 13 amino acids including 6 consecutive
XX histidine residues and a hG-CSF. E.coli transformed with recombinant
XX plasmid vector is useful for preparing hG-CSF. The method comprises
XX culturing the microorganism to obtain a hG-CSF fusion protein and
XX treating the fusion protein with a protease preferably factor Xa, to
XX obtain a hG-CSF, where the fusion protein is obtained from the culture by
XX employing Ni-column. The present sequence is human hG-CSF gene inserted
XX into plasmid p19CSFm
XX
XX Sequence 615 BP; 105 A; 219 C; 178 G; 113 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 523; DB 4; Length 615;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-107;
XX Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ACCCCCCCTGGGCGCTCCCTGCGCCAGAGCTCCCTGCTCAAGTGTAGAGCAA 60
XX
XX 88 ACCCCCTGGGCGCTCCAGCTCCCTGCGCCAGAGCTCCCTGCTCAAGTGTAGAGCAA 147
XX
XX 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGTCCAGGAGAGCTGTGTGCCACCTACAG 120
XX
XX 148 GTGAGGAAGATCCAGGGCGATGGCGAGCGTCCAGGAGAGCTGTGTGCCACCTACAG 207
XX
XX 121 CTGTGCCACCGAGAGCTGTGTGTGCTCGGACACTCTGTGGGCACTCCCTGGGCTCCC 180
XX

```

```

Db 208 CTGTGCCACCGCAGGAGCTGTGTGCTGCGACACTCTGTGGGCACTCCCTGGGCTCCC 267
QY 181 CTGAGCAGCTGCCCGCAGCAGCCCTGCAGCTGGCAGGCTGCTTTCAGCCAACTCCATAGC 240
Db 268 CTGAGCAGCTGCCCGCAGCAGCCCTGCAGCTGGCAGGCTGCTTTCAGCCAACTCCATAGC 327
QY 241 GGCCTTTTCTTACACAGGGGCTCTGAGGCCCTTGAAGGATCTCCCGAGTTGGGT 300
Db 328 GGCCTTTTCTTACACAGGGGCTCTGAGGCCCTTGAAGGATCTCCCGAGTTGGGT 387
QY 301 CCCACCTTGGACACACTGCAGCTGCAGCTGCGGACTTTGGCCACCACCATCTGGCAGCAG 360
Db 388 CCCACCTTGGACACACTGCAGCTGCGGACTTTGGCCACCACCATCTGGCAGCAG 447
QY 361 ATGGAAGAACTGGGAATGSCCTCTGAGCCCATCCAGGCTGCTTTCAGCCAACTCCATAGC 420
Db 448 ATGGAAGAACTGGGAATGSCCTCTGAGCCCATCCAGGCTGCTTTCAGCCAACTCCATAGC 507
QY 421 GCCTCTGCTTTCAGCGCGGCGGAGAGGGGTCTTAGTTGCTTCCCATCTGCAGAGCTTC 480
Db 508 GCCTCTGCTTTCAGCGCGGCGGAGAGGGGTCTTAGTTGCTTCCCATCTGCAGAGCTTC 567
QY 481 CTGGAGGTCTGTAACCGGCTTCTACGCCACCTTGGCCAGCCCT 523
Db 568 CTGGAGGTCTGTAACCGGCTTCTACGCCACCTTGGCCAGCCCT 610

RESULT 4
AAN70223
ID AAN70223 standard; DNA; 1520 BP.
XX
XX AAN70223;
XX
XX 25-MAR-2003 (revised)
XX 25-APR-1991 (first entry)
XX Plasmid pBRV2 insert.
XX
XX Human granulocyte colony stimulating factor; G-CSF; leukaemia; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 31..645
XX /tag= a
XX
XX EP220520-A.
XX
XX 06-MAY-1987.
XX
XX 30-SEP-1986; 86EP-00113446.
XX
XX 17-SEP-1985; 85JP-00206066.
XX 20-SEP-1985; 85JP-00209638.
XX 30-SEP-1985; 85JP-00217150.
XX 02-DEC-1985; 85JP-00269455.
XX 02-DEC-1985; 85JP-00269456.
XX 03-DEC-1985; 85JP-00270838.
XX 03-DEC-1985; 85JP-00270839.
XX 17-JUL-1986; 86JP-00166709.
XX 17-JUL-1986; 86JP-00166710.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Yamazaki T, Nagata S, Tsuchiya M;
XX
XX WPI; 1987-124182/18.
XX P-PSDB; AAP70162.
XX
XX Poly:peptide with human granulocyte colony stimulating factor activity -
XX is obtd. by cultivating transformant formed by recombinant DNA
XX procedures.
XX

```

PS Disclosure; Fig 4; 73pp; English.

XX The plasmid was isolated from a cDNA library prep'd. from CHU-2 cells, a
 CC human oral cavity tumour cell line, using a 1500 bp insert from pBSG4
 CC (AAN70222) and probe LC (AAN71351). The plasmid was used to prepare
 CC recombinant expression plasmids for the prodn. of h G-CSF. See also
 CC AAN70221-N70224 and AAN71349-N71351. (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 25-MAR-2003 to correct PI field.)

XX
 SQ Sequence 1520 BP; 303 A; 487 C; 402 G; 328 T; 0 U; 0 Other;

Query Match 100.0%; Score 523; DB 1; Length 1520;
 Best Local Similarity 100.0%; Pred. No. 2.5e-107;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
 Db 121 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 180

QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120
 Db 181 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 240

QY 121 CTGTGCGACCCGAGAGCTGTGTGTCTGCGACACTCTCTGGGATCCCTGGGCTCCC 180
 Db 241 CTGTGCGACCCGAGAGCTGTGTGTCTGCGACACTCTCTGGGATCCCTGGGCTCCC 300

QY 181 CTGAGCAGCTGCCAGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120
 Db 301 CTGAGCAGCTGCCAGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 240

QY 241 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 300
 Db 361 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 420

QY 301 CCCACCTTGGACACACTGCAGCTGGAGCTTCGCGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 360
 Db 421 CCCACCTTGGACACACTGCAGCTGGAGCTTCGCGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 480

QY 361 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 420
 Db 481 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 540

QY 421 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 480
 Db 541 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 600

QY 481 CTGGAGGTCTCTACCGGGGCTTCGAGAGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 523
 Db 601 CTGGAGGTCTCTACCGGGGCTTCGAGAGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 643

RESULT 5
 AAN71320
 ID AAN71320 standard; cDNA; 1520 BP.
 XX
 AC AAN71320;
 XX
 DT 23-APR-1991 (first entry)
 XX
 DE Sequence encoding human granulocyte colony stimulating factor (hGCSF) in
 DE pBRV2.
 XX
 KW Leukopenia therapy; neutropenia; eosinopenia; lymphopenia; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 31..120
 FT /*tag= a
 FT 121..645
 FT /*tag= b
 XX

PN EP217404-A.
 XX
 PD 08-APR-1987.
 XX
 PF 03-OCT-1986; 86EP-00113671.
 XX
 PR 04-OCT-1985; 85JP-00220450.
 XX
 PR 02-JUN-1986; 86JP-00125660.
 XX
 PA (CHUS) CHUGAI SEIVAKU KK.
 XX
 PI Tamura M, Nomura H, Hattori K, Ono M;
 XX WPI; 1987-095431/14.
 DR P-PSDB; AAP71384.
 XX
 PT Leukopenia treating agent esp. for producing fully mature neutrophils -
 PT contains human granulocyte colony stimulating factor obtd. by recombinant
 PT DNA methods etc.
 XX
 PS Claim 7; Fig 2; 34pp; English.
 XX
 CC The hGCSF has the following properties: (i) mol. wt. 19000 +/- 1000 (by
 CC SDS-PAGE); (ii) isoelectric pt. at 5.5, 5.8 or 6.1 each +/- 0.1; (iii) UV
 CC max. absorption at 280nm and min. at 250nm. Prodn. of the gene, vector
 CC etc. is described in JP 269455, 269456, 270838 and 270839, each of 1985
 CC
 SQ Sequence 1520 BP; 305 A; 488 C; 401 G; 326 T; 0 U; 0 Other;

Query Match 100.0%; Score 523; DB 1; Length 1520;
 Best Local Similarity 100.0%; Pred. No. 2.5e-107;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
 Db 121 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 180

QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120
 Db 181 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 240

QY 121 CTGTGCGACCCGAGAGCTGTGTGTCTGCGACACTCTCTGGGATCCCTGGGCTCCC 180
 Db 241 CTGTGCGACCCGAGAGCTGTGTGTCTGCGACACTCTCTGGGATCCCTGGGCTCCC 300

QY 181 CTGAGCAGCTGCCAGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120
 Db 301 CTGAGCAGCTGCCAGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 240

QY 241 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 300
 Db 361 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 420

QY 301 CCCACCTTGGACACACTGCAGCTGGAGCTTCGCGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 360
 Db 421 CCCACCTTGGACACACTGCAGCTGGAGCTTCGCGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 480

QY 361 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 420
 Db 481 ATGGAAGAACTGGGAATGGCCCTGCGCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 540

QY 421 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 480
 Db 541 GGCCTTTCTCTACCGGGGCTCCCTGCGAGCGCTTCGAGAGAGCTGTGTGCCACCTACAG 600

QY 481 CTGGAGGTCTCTACCGGGGCTTCGAGAGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 523
 Db 601 CTGGAGGTCTCTACCGGGGCTTCGAGAGAGCTTCGAGAGAGCTGTGTGCCACCTACAG 643

RESULT 6
 AAN60937
 ID AAN60937 standard; DNA; 1521 BP.

Db 421 CCCACCTTGGACACACTGCAGCTGCAGCTGCGGACTTTGCCACCCACCATCTGGCAGCAG 480
Qy 361 ATGCAAGAACTGGGAATGGCCCTGCTCCCTGCAGCCACCCAGGCTGCATGCCGGCCTTC 420
Db 481 ATGGAAGAACTGGGAATGGCCCTGCTCCCTGCAGCCACCCAGGCTGCATGCCGGCCTTC 540
Qy 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGCTCTAGTTGCCTCCCATCTGCGAGCTTC 480
Db 541 GCCTCTGCTTTCCAGCGCCGGGAGGAGGCTCTAGTTGCCTCCCATCTGCGAGCTTC 600
Qy 481 CTGAGGCTGCTGCTACCGGCTTACGCCACCTTGCACGACCT 523
Db 601 CTGAGGCTGCTGCTACCGGCTTACGCCACCTTGCACGACCT 643
RESULT 7
AAN81478
ID AAN81478 standard; cDNA; 1525 BP.
XX
AC AAN81478;
XX
DT 25-MAR-2003 (revised)
DT 14-DEC-1990 (first entry)
XX
DE Sequence encoding human granulocyte colony-stimulating factor (G-CSF) in
DE clone pP12 of MIA PaCa cDNA library.
XX
KW Leukaemia therapy; anaemia treatment; leukocyte; lymphokine;
KW interleukin-3; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS 43..132 Location/Qualifiers
FT /*tag= a
FT mat_peptide 133..657
FT /*tag= b
FT conflict 237..238
FT /*tag= c
FT /*note= "CHU-2 cDNA clones of Negata et al. contains a 9
FT conflict 588 base pair insertion (GTGATGGAG)"
FT /*tag= d
FT /*note= "G in the CHU-2 clone"
FT conflict 1237
FT /*tag= e
FT /*note= "C in the CHU-2 clone"
XX
EP256843-A.
XX
PD 24-FEB-1988.
XX
PF 11-AUG-1987; 87EP-00307114.
XX
PR 11-AUG-1986; 86US-00895154.
PR 18-NOV-1986; 86US-00932037.
XX
PA (CETU) CETUS CORP.
XX
PI Devlin JJ, Devlin PE., Kawaskai ES, Warren MK;
XX
XX WPI; 1988-051585/08.
DR P-PSDB; AAP81162.
XX
XX Human recombinant granulocyte colony-stimulating factor - causes
PT differentiation of granulocytes and monocytes from bone marrow progenitor
PT cells.
XX
PS Example; Fig 4; 61pp; English.
XX
CC The major difference between this clone and the CHU-2 cDNA clones of
CC Negata et al. (EMBO Journal 5:3,575-581(1986)) are given in FT of
CC AAN81478. The G-CSF was detected in purified mRNA fraction obtd. by

XX
AC AAN60937;
XX
DT 18-OCT-1991 (first entry)
XX
DE Plasmid pBRV2 insert encoding granulocyte CSF.
DE
KW G-CSF; granulocyte colony stimulating factor; antimicrobial.
XX
OS Synthetic.
XX
FH Key
FH CDS 31..645 Location/Qualifiers
FT /*tag= a
FT mat_peptide 121
FT /*tag= b
XX
WO6604506-A.
XX
PD 14-AUG-1986.
XX
PF 07-FEB-1986; 86WO-JP000053.
XX
PR 08-FEB-1985; 85JP-00023777.
PR 03-DEC-1985; 85JP-00270839.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
PA (ONOM/) ONO M.
XX
XX Ono M, Nomura H, Tamura M, Matsumoto M;
XX
XX WPI; 1986-225384/34.
DR P-PSDB; AAP61341.
XX
XX Infection-protection inducing agent - contains human granulocyte colony
XX stimulating factor obtd. by cell culture or recombinant technology.
XX
PS Disclosure; Fig 4; 139pp; Japanese.
XX
CC The plasmid encodes a novel polypeptide having human granulocyte colony
CC stimulating factor activity. The CSF may be produced either from a cell-
CC line secreting the factor into its medium, or from a transformant
CC microorganism. The product induces high immunity to infection by
CC anaerobic and aerobic bacteria and fungi
XX
SQ Sequence 1521 BP; 304 A; 488 C; 402 G; 327 T; 0 U; 0 Other;
Query Match 100.0%; Score 523; DB 1; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2.5e-107;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACCCCCTGGGCTGCGAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTAGAGCAA 60
Db 121 ACCCCCTGGGCTGCGAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTAGAGCAA 180
Qy 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
Db 181 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 240
Qy 121 CTGTGCCACCCGAGGAGCTGTGTGTCTCGGACCTCTGTGGCATCCCTGGGCTCCC 180
Db 241 CTGTGCCACCCGAGGAGCTGTGTGTCTCGGACCTCTGTGGCATCCCTGGGCTCCC 300
Qy 181 CTGAGCAGCTGCCAGCAGCGCTGTGAGCTGGCAGCTGCTTGAGCCAACTCCATAGC 240
Db 301 CTGAGCAGCTGCCAGCAGCGCTGTGAGCTGGCAGCTGCTTGAGCCAACTCCATAGC 360
Qy 241 GGCCTTTTCTTACAGGGCTCTGTGAGGCTTGGAGGAGTCTCCCGAGTTGGT 300
Db 361 GGCCTTTTCTTACAGGGCTCTGTGAGGCTTGGAGGAGTCTCCCGAGTTGGT 420
Qy 301 CCCACCTTGGACACACTGCAGCTGCAGCTGCGGACTTTGCCACCCACCATCTGGCAGCAG 360

CC sucrose density gradient centrifugation of induced MIA PaCa-2 cells as
 CC described in W06804607. (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 1525 BP; 303 A; 491 C; 402 G; 329 T; 0 U; 0 Other;

Query Match 100.0%; Score 523; DB 1; Length 1525;
 Best Local Similarity 100.0%; Pred. No. 2.5e-107;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTAGAGCAA 60
 Db 133 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTAGAGCAA 192
 QY 61 GTGAGAGATCCAGGGGATGGCCAGCGCTCCAGGAGAGCTGTGCCACCTACAG 120
 Db 193 GTGAGAGATCCAGGGGATGGCCAGCGCTCCAGGAGAGCTGTGCCACCTACAG 252
 QY 121 GTGTGCCACCCGAGGAGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
 Db 253 GTGTGCCACCCGAGGAGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 312
 QY 181 CTGACAGCTGCCCGAGCGCCCTGCAGTGGCAGCTCTTGAGCCAACTCATAGC 240
 Db 313 CTGACAGCTGCCCGAGCGCCCTGCAGTGGCAGCTCTTGAGCCAACTCATAGC 372
 QY 241 GGCCTTTTCTCTACAGGGGCTCTCGAGCGCTTGGAGGGATCTCCCGAGTTGGT 300
 Db 373 GGCCTTTTCTCTACAGGGGCTCTCGAGCGCTTGGAGGGATCTCCCGAGTTGGT 432
 QY 301 CCCACCTTGGACACACTGACGTGACGTCGTCCGAGCTTTGCCACCACTTGGCAGCAG 360
 Db 433 CCCACCTTGGACACACTGACGTGACGTCGTCCGAGCTTTGCCACCACTTGGCAGCAG 492
 QY 361 ATGGAAGAACTGGGAATGGCCCTGCAGCGCCACCCAGGCTGCCATGCCGCTTC 420
 Db 493 ATGGAAGAACTGGGAATGGCCCTGCAGCGCCACCCAGGCTGCCATGCCGCTTC 552
 QY 421 GCCTCTGCTTCCAGCGCGGGAGGAGGTCTAGTTCCTCCCACTGCAAGTTTC 480
 Db 553 GCCTCTGCTTCCAGCGCGGGAGGAGGTCTAGTTCCTCCCACTGCAAGTTTC 612
 QY 481 CTGAGAGTGTCTACCGGTTCTACGCCACCTTGGCCAGCCCT 523
 Db 613 CTGAGAGTGTCTACCGGTTCTACGCCACCTTGGCCAGCCCT 655

RESULT 8
 AAN91086

ID AAN91086 standard; DNA; 1525 BP.

XX AC AAN91086;

XX DT 04-JUL-1990 (first entry)

XX DE Plasmid pP12 contg. colony stimulating factor-1 gene.

XX KW Colony stimulating factor-1; pP12; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT sig_peptide 43..132

XX FT mat_peptide 133..654

XX FT /*tag= a

XX FT /*tag= b

XX XX W06901038-A.

XX XX 09-FEB-1989.

XX XX 20-JUL-1988; 88WO-US002445.

XX

PR 24-JUL-1987; 87US-00077188.

XX PA (CETU) CETUS CORP.

XX PI Kawasaki ES, Devlin JJ, Martin G, O'rouke E, Clark R;

XX WPI; 1989-061174/08.

XX DR P-PSDB; AAP95033.

XX PT Recombinant Baculovirus transfer vectors - used for prodn. of colony
 stimulating factor in Baculovirus-insect cell expression system.

XX PS Disclosure; Fig 3; 68pp; English.

XX CC The cDNA insert of pP12 contains 11 more bases than the CHU-2 G-CSF
 clone. The major difference between this clone, derived from MIA PaCa-2,
 and CHU-2 clone is a 9 bp insertion in the CHU-2 clone between bases 237
 and 238. There are two other differences: an A at position 588 (G in the
 CHU-2 clone) is a silent third base change, and a T at position 1237 (C in
 the CHU-2 clone) in the 3' untranslated region. See also AAN91085

XX SQ Sequence 1525 BP; 303 A; 490 C; 403 G; 328 T; 0 U; 1 Other;

Query Match 100.0%; Score 523; DB 1; Length 1525;

Best Local Similarity 100.0%; Pred. No. 2.5e-107;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTAGAGCAA 60
 Db 133 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTCTAGAGCAA 192
 QY 61 GTGAGAGATCCAGGGGATGGCCAGCGCTCCAGGAGAGCTGTGCCACCTACAG 120
 Db 193 GTGAGAGATCCAGGGGATGGCCAGCGCTCCAGGAGAGCTGTGCCACCTACAG 252
 QY 121 CTGTGCCACCCGAGGAGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
 Db 253 CTGTGCCACCCGAGGAGTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 312
 QY 181 CTGACAGCTGCCCGAGCGCCCTGCAGTGGCAGCTCTTGAGCCAACTCATAGC 240
 Db 313 CTGACAGCTGCCCGAGCGCCCTGCAGTGGCAGCTCTTGAGCCAACTCATAGC 372
 QY 241 GGCCTTTTCTCTACAGGGGCTCTCGAGCGCTTGGAGGGATCTCCCGAGTTGGT 300
 Db 373 GGCCTTTTCTCTACAGGGGCTCTCGAGCGCTTGGAGGGATCTCCCGAGTTGGT 432
 QY 301 CCCACCTTGGACACACTGACGTGACGTCGTCCGAGCTTTGCCACCACTTGGCAGCAG 360
 Db 433 CCCACCTTGGACACACTGACGTGACGTCGTCCGAGCTTTGCCACCACTTGGCAGCAG 492
 QY 361 ATGGAAGAACTGGGAATGGCCCTGCAGCGCCACCCAGGCTGCCATGCCGCTTC 420
 Db 493 ATGGAAGAACTGGGAATGGCCCTGCAGCGCCACCCAGGCTGCCATGCCGCTTC 552
 QY 421 GCCTCTGCTTCCAGCGCGGGAGGAGGTCTAGTTCCTCCCACTGCAAGTTTC 480
 Db 553 GCCTCTGCTTCCAGCGCGGGAGGAGGTCTAGTTCCTCCCACTGCAAGTTTC 612
 QY 481 CTGAGAGTGTCTACCGGTTCTACGCCACCTTGGCCAGCCCT 523
 Db 613 CTGAGAGTGTCTACCGGTTCTACGCCACCTTGGCCAGCCCT 655

RESULT 9
 ACC78869

ID ACC78869 standard; DNA; 525 BP.

XX AC ACC78869;

XX DT 02-SEP-2003 (first entry)

XX DE Human granulocyte colony stimulating factor (G-CSF) encoding DNA.

XX Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
KW granulocyte colony stimulating factor; G-CSF; human; gene; ds.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 1..525
FT /*tag= a
FT /product= "G-CSF"
XX WO2003031464-A2.
XX 17-APR-2003.
XX 09-OCT-2002; 2002WO-US032263.
XX 10-OCT-2001; 2001US-0328523P.
XX 19-OCT-2001; 2001US-0344692P.
XX 28-NOV-2001; 2001US-0334233P.
XX 28-NOV-2001; 2001US-0334301P.
XX 07-JUN-2002; 2002US-0367292P.
XX 25-JUN-2002; 2002US-0391777P.
XX 17-JUL-2002; 2002US-0396594P.
XX 16-AUG-2002; 2002US-0404249P.
XX 28-AUG-2002; 2002US-0407527P.
XX (NEOS-) NEOSE TECHNOLOGIES INC.
XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX WPI; 2003-449162/42.
XX P-PSDB; ABR55839.
XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to
PT form truncated glycan, and adding or deleting glycosyl groups to a
PT peptide and/or adding modifying group of a peptide to remodel the
PT peptide.
XX Example; Fig 52; 900pp; English.
XX The invention relates to a cell-free, in vitro method of remodeling a
CC peptide. The method involves removing a saccharyl subunit from the
CC peptide, thus forming a truncated glycan, and contacting the truncated
CC glycan with at least one glycosyltransferase and at least one glycosyl
CC donor under conditions suitable to transfer at least one glycosyl donor
CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
CC interferon alpha peptide, interferon beta peptide, Factor VIII peptide,
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC glycoprotein IIB/IIIa monoclonal antibody peptide, chimeric anti-HER2
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC hormone (hGH) peptide, and a modifying group, where the modifying group
CC is covalently attached to the peptide through an intact glycosyl linking
CC group. The method is useful for a cell-free, in vitro method of
CC remodeling the above mentioned peptides. The present sequence represents
XX a human G-CSF encoding DNA
SQ Sequence 525 BP; 84 A; 192 C; 152 G; 97 T; 0 U; 0 Other;
Query Match 99.7%; Score 521.4; DB 7; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.9e-107;
Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTGTAGACAA 60
|||||

DB 1 ACCCCCTGGGCGCTCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTGTAGACAA 60
QY 61 GTGAGGAATCCAGGCGGATGGCGAGCGCTCCAGAGAGAGCTGTGTGCCACTTACAAAG 120
DB 61 GTGAGGAATCCAGGCGGATGGCGAGCGCTCCAGAGAGAGCTGTGTGCCACTTACAAAG 120
QY 121 CTGTGCCACCCCGAGGAGCTGTGTCTCGGACACTCTCTGTGGCACTCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCCGAGGAGCTGTGTCTCGGACACTCTCTGTGGCACTCCCTGGGCTCCC 180
QY 181 CTGAGCAGCTGCCCGAGGAGCTGTGTCTCGGACACTCTCTGTGGCACTCCCTGGGCTCCC 240
DB 181 CTGAGCAGCTGCCCGAGGAGCTGTGTCTCGGACACTCTCTGTGGCACTCCCTGGGCTCCC 240
QY 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGGCGCTCTGGAAGGATCTCCCGAGTGGGT 300
DB 241 GGCCTTTTCTCTACAGGGGCTCTCTGAGGCGCTCTGGAAGGATCTCCCGAGTGGGT 300
QY 301 CCCACTTGGACACACTGAGTGAGCTGCGGAGCTTGGCCACCATCTGGCAGCAG 360
DB 301 CCCACTTGGACACACTGAGTGAGCTGCGGAGCTTGGCCACCATCTGGCAGCAG 360
QY 361 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCACCCAGGGTGCCATGCCGCTTC 420
DB 361 ATGGAAGAACTGGGAATGCGCCCTGCGAGCCACCCAGGGTGCCATGCCGCTTC 420
QY 421 GCCTCTGCTTCCAGCGCGGAGAGGGGTCTAGTTGCTCCCATCTGCAGAGCTTC 480
DB 421 GCCTCTGCTTCCAGCGCGGAGAGGGGTCTAGTTGCTCCCATCTGCAGAGCTTC 480
QY 481 CTGAGGAGTGTCTAGCGGTCTCTAGCCACCTTGCCAGCCCT 523
DB 481 CTGAGGAGTGTCTAGCGGTCTCTAGCCACCTTGCCAGCCCT 523
RESULT 10
ABR94177
ID ABR94177 standard; cDNA; 549 BP.
XX
AC ABA94177;
XX
DT 08-MAY-2002 (first entry)
XX
DE Granulocyte colony stimulating factor related nucleotide sequence.
XX
KW Granulocyte colony stimulating factor; G-CSF; gene; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1..549
FT /*tag= a
FT /partial
FT /product= "G-CSF"
FT /note= "no start codon given"
XX
XX KE98077885-A.
XX
XX 16-NOV-1998.
XX
XX 23-APR-1997; 97KR-00015210.
XX
XX 23-APR-1997; 97KR-00015210.
XX
XX (MOKA-) MOKAM LIFE SCI RES CENT.
XX
XX Sohn YD, Lee EG, Kim SH, Park DH;
XX
XX WPI; 2000-035728/03.
XX
XX P-PSDB; ABB05960.
XX
XX Recombinant microorganism expressing granulocyte colony stimulating
PT factor and process for preparing the recombinant protein therefrom.
PT

XX Disclosure; Page 11; 16pp; Korean.

XX The present invention describes a recombinant microorganism expressing a

CC granulocyte colony stimulating factor (G-CSF), and process for preparing

CC the recombinant protein. The present sequence encodes a G-CSF related

CC protein, which is given in the exemplification of the present invention

XX Sequence 549 BP; 90 A; 199 C; 160 G; 100 T; 0 U; 0 Other;

Query Match 99.7%; Score 521.4; DB 3; Length 549;

Best Local Similarity 99.8%; Pred. No. 5e-107;

Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTCCAGCTCCCTGCCCGCAGAGTTCCTGCTCAAGTGTAGAGCAA 60

DB 25 ACCCCCTGGGCTCCAGCTCCCTGCCCGCAGAGTTCCTGCTCAAGTGTAGAGCAA 84

QY 61 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTCACCTACAA 120

DB 85 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTCACCTACAA 144

QY 121 CTGTGCCACCCGAGAGTGTGTCTGTCTGGACACTCTCTGGGATCCCTGGGCTCCC 180

DB 145 CTGTGCCACCCGAGAGTGTGTCTGTCTGGACACTCTCTGGGATCCCTGGGCTCCC 204

QY 181 CTGAGCAGCTGCCCGCAGCGCTCCAGCTGGCAGGCTGTGTCAGCAACTCCATAGC 240

DB 205 CTGAGCAGCTGCCCGCAGCGCTCCAGCTGGCAGGCTGTGTCAGCAACTCCATAGC 264

QY 241 GGCCTTTTCTTACAGGGGTCTCTGAGGCGCTTGGAGGATCTCCCGAGTTGGGT 300

DB 265 GGCCTTTTCTTACAGGGGTCTCTGAGGCGCTTGGAGGATCTCCCGAGTTGGGT 324

QY 301 CCCACTTGGACACACTGAGCTGAGCTGCCGACTTGTGCACCACTCTGCGAGCAG 360

DB 325 CCCACTTGGACACACTGAGCTGAGCTGCCGACTTGTGCACCACTCTGCGAGCAG 384

QY 361 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGCTGCATGCCGCTTC 420

DB 385 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGCTGCATGCCGCTTC 444

QY 421 GCCTCTGCTTCCAGCGCGGGCAGGAGGGTCTAGTTGCTTCCATCTCGAGCTTC 480

DB 445 GCCTCTGCTTCCAGCGCGGGCAGGAGGGTCTAGTTGCTTCCATCTCGAGCTTC 504

QY 481 CTGGAGGTGTCTAGCGGTCTTACGCCACCTTGGCCAGCCCT 523

DB 505 CTGGAGGTGTCTAGCGGTCTTACGCCACCTTGGCCAGCCCT 547

RESULT 11

ID AAN71089

AC AAN71089 standard; DNA; 1415 BP.

XX AAN71089;

DT 25-MAR-2003 (revised)

DT 26-APR-1991 (first entry)

XX Sequence of human granulocyte colony stimulating factor (hpg-CSF) cDNA

DE clone Ppo2.

XX Haematopoietic disorders; therapy; aplastic anaemia;

KW bone marrow transplant; burn wounds; leukaemia; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

PH 1..36

FT CDS

XX mat_peptide

FT 37..561

FT /*tag= a

FT /*tag= b

FT polyA_signal 1797..1802

FT /*tag= c

XX W08701132-A.

XX 26-FEB-1987.

XX 22-AUG-1986; 86WO-US001708.

XX 23-AUG-1985; 85US-00768954.

XX 23-AUG-1985; 85US-00768959.

XX 03-MAR-1986; 86US-00835548.

XX (KIRI) KIRIN AMGEN INC.

XX (KIRI) KIRIN AMGEN INC.

XX (AMGE-) AMGEN.

XX Souza LM;

XX WPI; 1987-064855/09.

XX P-PSDB; AAP70730.

XX Poly:peptide with granulocyte colony stimulating factor activity - obt'd.

XX by recombinant DNA procedures for treating haematopoietic disorders.

XX Disclosure; Page 22-24; 79pp; English.

XX The examples describe procedures for the designing of probes for hpg-CSF

CC cDNA and genomic clones, both of which are claimed. Specifically claimed

CC are DNA sequences encoding for (Ala 1)hpg-CSF; (Ser 36, 42, 64 and 74)hpg

CC -CSF and the corresponding Met-1 cpds. The novelty is that hpg-CSF is the

CC prod. of prokaryotic or eucaryotic expression of an exogenous DNA

CC sequence. The construction of hpg-CSF expression vectors is also

CC described in the examples. (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1415 BP; 265 A; 451 C; 380 G; 319 T; 0 U; 0 Other;

Query Match 99.7%; Score 521.4; DB 1; Length 1415;

Best Local Similarity 99.8%; Pred. No. 5.6e-107;

Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCTCCAGCTCCCTGCCCGCAGAGTTCCTGCTCAAGTGTAGAGCAA 60

DB 37 ACCCCCTGGGCTCCAGCTCCCTGCCCGCAGAGTTCCTGCTCAAGTGTAGAGCAA 96

QY 61 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTCACCTACAA 120

DB 97 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTCACCTACAA 156

QY 121 CTGTGCCACCCGAGAGTGTGTGTCGACACTCTCTGGGATCCCTGGGCTCCC 180

DB 157 CTGTGCCACCCGAGAGTGTGTGTCGACACTCTCTGGGATCCCTGGGCTCCC 216

QY 181 CTGAGCAGCTGCCCGCAGCGCTCCAGCTGGCAGGCTGTGTCAGCAACTCCATAGC 240

DB 217 CTGAGCAGCTGCCCGCAGCGCTCCAGCTGGCAGGCTGTGTCAGCAACTCCATAGC 276

QY 241 GGCCTTTTCTTACAGGGGTCTCTGAGGCGCTTGGAGGATCTCCCGAGTTGGGT 300

DB 277 GGCCTTTTCTTACAGGGGTCTCTGAGGCGCTTGGAGGATCTCCCGAGTTGGGT 336

QY 301 CCCACTTGGACACACTGAGCTGAGCTGCCGACTTGTGCACCACTCTGCGAGCAG 360

DB 337 CCCACTTGGACACACTGAGCTGAGCTGCCGACTTGTGCACCACTCTGCGAGCAG 396

QY 361 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGCTGCATGCCGCTTC 420

DB 397 ATGGAAGAACTGGGAATGGCCCTCCCTGCGAGCCACCCAGGCTGCATGCCGCTTC 456

QY 421 GCCTCTGCTTCCAGCGCGGGCAGGAGGGTCTAGTTGCTTCCATCTCGAGCTTC 480

DB 457 GCCTCTGCTTCCAGCGCGGGCAGGAGGGTCTAGTTGCTTCCATCTCGAGCTTC 516

QY 481 CTGAGGTTGTCACCGGTTCTACGCCACCTTCCCGAGCCCT 523
Db |||||
517 CTGAGGTTGTCACCGGTTCTACGCCACCTTCCCGAGCCCT 559

RESULT 12

ABX63825

ID ABX63825 standard; cDNA; 1508 BP.

XX AC ABX63825;

XX DT 26-FEB-2003 (first entry)

XX DE Human cDNA #925 differentially expressed in activated vascular tissue.

XX KW Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
KW hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
KW gene therapy; vascular disease; cancer; coronary; artery disease;
KW hypertension; diabetes; pre-eclampsia; restenosis;
KW ischaemia-reperfusion injury; stroke.

XX OS Homo sapiens.

XX XX US2002137081-A1.

XX PN 26-SEP-2002.

XX PD 08-JAN-2002; 2002US-00044090.

XX PF 28-JUL-2000; 2000US-0222469P.

XX PR 08-JAN-2001; 2001US-0260483P.

XX PA (BAND/) BANDMAN O.

XX PI Bandman O;

XX DR WPI; 2003-110597/10.

XX PT Combination for diagnosing, staging, treating, or monitoring the
PT progression of treatment of a vascular disease, e.g. atherosclerosis,
PT comprises several cDNAs that are differentially expressed in activated
PT vascular tissue.

XX PS Claim 1; Page; 18pp; English.

XX CC This invention relates to a combination comprising several cDNAs that are
XX differentially expressed in activated vascular tissue. The invention also
XX discloses a high throughput method for detecting differentially expressed
XX cDNAs in a sample. The cDNAs of the invention may have
XX antiatherosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
XX gynaecological; vasotropic and cerebroprotective activities and may be
XX used in gene therapy. The cDNAs of the invention may be used in a high-
XX throughput methods for detecting differential expression of one or more
XX cDNAs in a sample, or screening several molecules or compounds to
XX identify a molecule or compound that specifically binds a cDNA of the
XX invention. A protein encoded by the cDNA may be used to screen several
XX molecules or compounds to identify a ligand that specifically binds to
XX the protein, or to produce or purify an antibody to the protein that can
XX be used to detect a protein in a sample or purify a natural or
XX recombinant protein from a sample. The nucleotides may be useful for
XX diagnosing, staging, treating or monitoring the progression of treatment
XX of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
XX disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion
XX injury, restenosis, or stroke. The cDNAs can also be used for large-scale
XX genetic or gene expression analysis of several new nucleic acid
XX molecules. Antibodies to the proteins encoded by the cDNAs are useful for
XX diagnosing pre-pathologic disorders, and chronic or acute diseases
XX associated with abnormalities in the expression, amount or distribution
XX of the protein. The present sequence represents a cDNA of the invention
XX that is differentially expressed in activated vascular tissue. Note: The
XX sequence data for this patent did not form part of the specification, but
XX was obtained in electronic format directly from USPTO at

CC http.seqdata.uspto.gov/sequence.html?DocID=20020137081

XX Sequence 1508 BP; 294 A; 484 C; 402 G; 328 T; 0 U; 0 Other;

SQ Query Match 99.7%; Score 521.4; DB 7; Length 1508;

Best Local Similarity 99.8%; Pred. No. 5.6e-107;

Matches 522; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTCTTAGAGCAA 60

Db 114 ACCCCCTGGGCGCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTGTCTTAGAGCAA 173

QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120

Db 174 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 233

QY 121 CTGTGCCACCCGAGAGCTGTGTGTCTCGACACTCTCTGGGATCCCTGGGCTCC 180

Db 234 CTGTGCCACCCGAGAGCTGTGTGTCTCGACACTCTCTGGGATCCCTGGGCTCC 293

QY 181 CTGAGCAGCTGCCCGAGCGCTCCAGGCGCTGAGCTGGCAGGCTGTGTGAGCAACTCCATAGC 240

Db 294 CTGAGCAGCTGCCCGAGCGCTCCAGGCGCTGAGCTGGCAGGCTGTGTGAGCAACTCCATAGC 353

QY 241 GGCCTTTTCTCTACAGGGGCTCTGAGGCGCTGGAGGATCTCCCGAGTTGGT 300

Db 354 GGCCTTTTCTCTACAGGGGCTCTGAGGCGCTGGAGGATCTCTCCCGAGTTGGT 413

QY 301 CCCACCTTGGACACACTGACGCTGGACGCTGCGCGGCTTTGCCACCACTCTGGCAGCAG 360

Db 414 CCCACCTTGGACACACTGACGCTGGACGCTGCGCGGCTTTGCCACCACTCTGGCAGCAG 473

QY 361 ATGGAAGAACTGGGAATGCGCTGCGCTGAGCGCGCTGAGCGGCTGCCATGCGGCGCTTC 420

Db 474 ATGGAAGAACTGGGAATGCGCTGCGCTGAGCGCGCTGAGCGGCTGCCATGCGGCGCTTC 533

QY 421 GCCTCTGCTTTCACGCGCGGCGAGGCGCTCTAGTTGCTCCCTCCCATCTGCAGAGCTTC 480

Db 534 GCCTCTGCTTTCACGCGCGGCGAGGCGCTCTAGTTGCTCCCTCCCATCTGCAGAGCTTC 593

QY 481 CTGAGGTTGTCACCGGTTCTACGCCACCTTCCCGAGCCCT 523

Db 594 CTGAGGTTGTCACCGGTTCTACGCCACCTTCCCGAGCCCT 636

RESULT 13

AAI71848

ID AAI71848 standard; cDNA; 644 BP.

XX AC AAI71848;

XX DT 07-JAN-2002 (first entry)

XX DE Recombinant human granulocyte colony stimulating factor cDNA.

XX KW Human; granulocyte colony stimulating factor; rhG-CSF; recombinant; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 94..621

FT FT /*tag= a

FT FT /product= "rhG-CSF"

XX CN1167150-A.

XX PD 10-DEC-1997.

XX PF 05-JUN-1996; 96CN-00106418.

XX PR 05-JUN-1996; 96CN-00106418.

XX XX (JIUY-) JIUYAN GENE ENG CO LTD HANGZHOU.

```

XX PI Su Y, Kong T, Wang C;
XX DR WPI; 2001-590346/67.
XX DR P-PSDB; AAMS1536.
XX PT Production of recombined human granulocyte colony stimulation factor.
XX PS Disclosure; Page 8 (disclosure); 15pp; Chinese.
XX CC The invention relates to a method for producing recombinant human
CC granulocyte colony stimulating factor (rhG-CSF). The method includes the
CC following steps: (a) reverse transcription-polymerase chain reaction of
CC the human granulocyte colony stimulating factor gene; (b) transforming
CC Escherichia coli; (c) renaturation of protein by hollow fibre
CC ultrafiltration dialysis; (d) passing the renatured protein through ion
CC exchange chromatography, hydrophobic chromatography and molecular sieve
CC chromatography which are combined together sequentially; and (e)
CC purifying so to obtain a high yield of high-purity medicinal rhG-CSF
CC protein. The present sequence encodes rhG-CSF
XX SQ Sequence 644 BP; 128 A; 216 C; 172 G; 128 T; 0 U; 0 Other;

Query Match 98.2%; Score 513.4; DB 5; Length 644;
Best Local Similarity 98.9%; Pred. No. 3.1e-105;
Matches 517; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
DB |||
DB 97 ACACCATTAGCCCTGCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 156
QY 61 GTGAGGAAGATCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAAG 120
DB |||
DB 157 GTGAGGAAGATCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAAG 216
QY 121 CTGTGCCACCCGAGAGCTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB |||
DB 217 CTGTGCCACCCGAGAGCTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 276
QY 181 CTGAGCAGCTGCCAGCCAGCCCTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 240
DB |||
DB 277 CTGAGCAGCTGCCAGCCAGCCCTCGAGCTGGCAGGCTGTGTGAGCCAACTCCATAGC 336
QY 241 GGCCTTTTCTTACAGGGGTCTCTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 300
DB |||
DB 337 GGCCTTTTCTTACAGGGGTCTCTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 396
QY 301 CCCACCTTGGACACACTGCAGCTGGACGTCGCGGACTTTGCCACCACTCTGGCAGCAG 360
DB |||
DB 397 CCCACCTTGGACACACTGCAGCTGGACGTCGCGGACTTTGCCACCACTCTGGCAGCAG 456
QY 361 ATGGAAGAACTGGGAATGCCCTCGCTGCGAGCCACCCAGGGTGCATGCCGCGCTTC 420
DB |||
DB 457 ATGGAAGAACTGGGAATGCCCTCGCTGCGAGCCACCCAGGGTGCATGCCGCGCTTC 516
QY 421 GCCTCTGCTTTTCAGCGCGGCGAGAGGGTCTAGTTGCTCCCATCTCGAGAGCTTC 480
DB |||
DB 517 GCCTCTGCTTTTCAGCGCGGCGAGAGGGTCTAGTTGCTCCCATCTCGAGAGCTTC 576
QY 481 CTGAGAGGTGTCTTACCGGTTTCTACGCCACCTTGGCCAGCCCT 523
DB |||
DB 577 CTGAGAGGTGTCTTACCGGTTTCTACGCCACCTTGGCCAGCCCT 619

RESULT 14
AAZ21169
XX ID AAZ21169 standard; cDNA; 540 BP.
XX AC AAZ21169;
XX AC AAZ21169;
XX DT 19-NOV-1999 (first entry)
XX DE Recombinant human granulocyte colony stimulating factor encoding cDNA.

```

```

XX Human; granulocyte colony stimulating factor; G-CSF; rhG-CSF; ss.
XX KW Homo sapiens.
XX OS Synthetic.
XX FH Key
XX CDS Location/Qualifiers
FT 1..540
FT /*tag= a
FT /product= "recombinant human G-CSF"
FT /transl_except= (pos:13..15,aa:Xaa)
FT /note= "Xaa represents nothing i.e. nothing is given in
FT the protein at this position"
FT misc_difference 1..12
FT /*tag= b
FT /note= "this part of the sequence encodes a 4 amino acid
FT peptide not present in the wild type protein"
FT misc_difference 64..66
FT /*tag= c
FT /note= "alternatively TGC at this position is replaced by
FT GCC causing an Ala residue to replace Cys in the protein"
XX CNI217342-A.
XX 26-MAY-1999.
XX 19-NOV-1997; 97CN-00123162.
XX 19-NOV-1997; 97CN-00123162.
XX (JIAN') JIANG Y.
XX Jiang Y, Dai W;
XX WPI; 1999-459246/39.
XX P-PSDB; AAY29929.
XX Colony stimulating factor for recombination of human granulocytes -
XX obtained by adding 3-6 amino acid residues at N end of its sequence, in
XX which at least one amino acid residue is arginine.
XX Claim 1; Fig 1; 15pp; Chinese.
XX The present sequence encodes a recombinant human granulocyte colony
XX stimulating factor (rhG-CSF). The present invention describes rhG-CSF
XX proteins which are obtained by adding 3-6 amino acid residues at the N-
XX terminal of the rhG-CSF sequence, in which at least one amino acid residue
XX is arginine. Preferably adding 4-6 amino acid residues including the
XX sequence of methionine, arginine, glutamic acid and serine at the N-
XX terminal. Also described are the related sequence, expression carrier,
XX host cell and medicinal composition. The activity of the recombinant
XX protein is increased and its stability is increased
XX SQ Sequence 540 BP; 90 A; 191 C; 158 G; 101 T; 0 U; 0 Other;

Query Match 97.6%; Score 510.2; DB 2; Length 540;
Best Local Similarity 98.5%; Pred. No. 1.6e-104;
Matches 515; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
DB |||
DB 16 ACCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 75
QY 61 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 120
DB |||
DB 76 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAG 135
QY 121 CTGTGCCACCCGAGAGCTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
DB |||
DB 136 CTGTGCCACCCGAGAGCTGTGTCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 195
QY 181 CTGAGCAGCTGCCAGCCAGCCCTCGAGCTGGGAGGCTGTGTGAGCCAACTCCATAGC 240
DB |||

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 21:23:54 ; Search time 2723.62 Seconds
(without alignments)
8322.904 Million cell updates/sec

Title: US-10-009-792C-18_COPY_88_610

Perfect score: 523
Sequence: 1 acccccctggccctgcag.....acgcacacttgcacagccct 523

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba.*
- 2: gb_bt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hg_hum.*
- 31: em_hg_inv.*
- 32: em_hg_other.*
- 33: em_hg_mus.*
- 34: em_hg_pln.*
- 35: em_hg_rtd.*
- 36: em_hg_mam.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	100.0	525	6	AR024358
2	523	100.0	525	6	AR024358 Sequence
3	523	100.0	525	6	AR091731
4	523	100.0	525	6	AR091731 Sequence
5	523	100.0	525	6	E01731 cDNA encodi
6	523	100.0	525	6	E02573 DNA encodin
7	523	100.0	525	6	E07164 CDNA encodi
8	523	100.0	525	6	E09431 CDNA encodi
9	523	100.0	525	6	E15131 Human mRNA
10	523	100.0	525	6	E17150 Human mRNA
11	523	100.0	525	6	I83709 Sequence 1
12	523	100.0	525	6	I83709 Sequence 1
13	523	100.0	525	6	AR363055 Sequence
14	523	100.0	525	6	AR363055 Sequence
15	523	100.0	525	6	HUMGCSF
16	523	100.0	525	6	HUMGCSF
17	521.4	99.7	1671	9	HUMGCSF
18	521.4	99.7	1671	9	HUMGCSF
19	520.4	99.5	522	6	EC033245
20	520.4	99.5	522	6	EC033245
21	519.8	99.4	1415	6	E01631
22	519.8	99.4	1415	6	E01631
23	519.8	99.4	1415	6	E37811
24	519.8	99.4	1415	6	E37811
25	510.2	97.6	541	6	I01623
26	510.2	97.6	541	6	I01623
27	510.2	97.6	2382	6	BD000076
28	510.2	97.6	2382	6	BD000076
29	509.2	97.4	2455	6	BD178096
30	509.2	97.4	2455	6	BD178096
31	509.2	97.4	2455	6	A76867
32	507	96.9	525	6	A76867
33	506	96.7	522	6	AR123945
34	506	96.7	522	6	AR123945
35	504.4	96.4	522	6	AX398641
36	504.4	96.4	522	6	AX398641
37	504.4	96.4	522	6	AX398637
38	504.4	96.4	522	6	AX398637
39	504.2	96.4	519	6	AX398639
40	504.2	96.4	519	6	AX398639
41	503.8	96.3	546	6	AX027604
42	503.8	96.3	546	6	AX027604
43	503.8	96.3	921	6	AX027606
44	503.8	96.3	921	6	AX027606
45	503.8	96.3	921	6	AR202281
					AR202281
					AR202283
					AR202283
					AR202223
					AR202223
					AR202226
					AR202226
					AR202229
					AR202229
					AR223225
					AR223225

ALIGNMENTS

RESULT 1	AR024358	525 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	Sequence 1 from patent US 5795968				
DEFINITION	Sequence 1 from patent US 5795968				
ACCESSION	AR024358				
VERSION	AR024358.1	GI:3977652			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 525)				
AUTHORS	Ruga, T., Miyaji, H., Sato, M., Okabe, M., Morimoto, M., Itoh, S.,				
TITLE	Yamasaki, M., Yokoo, Y., Yamaguchi, K., Yoshida, H. and Konatsu, Y.				
	Polypeptide derivatives of human granulocyte colony stimulating				
	factor				

JOURNAL Patent: US 5795968-A 1 18-AUG-1998;

FEATURES Location/Qualifiers

source 1..525

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 525;
Best Local Similarity 100.0%; Pred No. 2,5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCCCCTGGCCCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA 60
Db 1 ACCCCCTGGCCCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA 60
Qy 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
Db 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
Qy 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
Db 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
Qy 181 CTGAGCAGCTGCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 240
Db 181 CTGAGCAGCTGCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 240
Qy 241 GGCCTTTTCTCTACAGGGGCTCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 300
Db 241 GGCCTTTTCTCTACAGGGGCTCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 300
Qy 301 CCCACCTTGGACACACTGCGAGCTGGAGCTCGCGACCTTTGCCACCACTTGGCGAGCAG 360
Db 301 CCCACCTTGGACACACTGCGAGCTGGAGCTCGCGACCTTTGCCACCACTTGGCGAGCAG 360
Qy 361 ATGGAAGAACTGGGAATGGGCTGCGGCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 420
Db 361 ATGGAAGAACTGGGAATGGGCTGCGGCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 420
Qy 421 GCCTCTGCTTTCCAGCGCCCGGCGAGGAGGCTCTAGTTGCTCCATCTGCAGAGCTTC 480
Db 421 GCCTCTGCTTTCCAGCGCCCGGCGAGGAGGCTCTAGTTGCTCCATCTGCAGAGCTTC 480
Qy 481 CTGAGGTGTCGTACCGCTTCTACGCCACCTTGCCAGCCCT 523
Db 481 CTGAGGTGTCGTACCGCTTCTACGCCACCTTGCCAGCCCT 523

RESULT 2

LOCUS AR091731 525 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 594518.
ACCESSION AR091731
VERSION AR091731.1 GI:10018485
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 525)
AUTHORS Kuga,T., Miyaji,H., Sato,M., Okabe,M., Morimoto,M., Itoh,S., Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.
TITLE Method of producing a polypeptide having human granulocyte colony stimulating factor activity
JOURNAL Patent: US 594518-A 1 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..525
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 525;
Best Local Similarity 100.0%; Pred No. 2,5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCCCCTGGCCCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA 60
Db 1 ACCCCCTGGCCCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA 60
Qy 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
Db 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAG 120
Qy 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
Db 121 CTGTGCCACCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 180
Qy 181 CTGAGCAGCTGCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 240
Db 181 CTGAGCAGCTGCCCGAGGAGCTGTGTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCC 240
Qy 241 GGCCTTTTCTCTACAGGGGCTCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 300
Db 241 GGCCTTTTCTCTACAGGGGCTCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 300
Qy 301 CCCACCTTGGACACACTGCGAGCTGGAGCTCGCGACCTTTGCCACCACTTGGCGAGCAG 360
Db 301 CCCACCTTGGACACACTGCGAGCTGGAGCTCGCGACCTTTGCCACCACTTGGCGAGCAG 360
Qy 361 ATGGAAGAACTGGGAATGGGCTGCGGCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 420
Db 361 ATGGAAGAACTGGGAATGGGCTGCGGCTGCGAGGCTCGGAGGATCTCCCGAGTTGGGT 420
Qy 421 GCCTCTGCTTTCCAGCGCCCGGCGAGGAGGCTCTAGTTGCTCCATCTGCAGAGCTTC 480
Db 421 GCCTCTGCTTTCCAGCGCCCGGCGAGGAGGCTCTAGTTGCTCCATCTGCAGAGCTTC 480
Qy 481 CTGAGGTGTCGTACCGCTTCTACGCCACCTTGCCAGCCCT 523
Db 481 CTGAGGTGTCGTACCGCTTCTACGCCACCTTGCCAGCCCT 523

RESULT 3

LOCUS E01731 525 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding hg-CSF form human peripheral macrophage.
ACCESSION E01731
VERSION E01731.1 GI:2169984
KEYWORDS JP 1988267292-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 525)
AUTHORS Kuga,T., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M., Itoh,S., Yamasaki,M., Yokoo,Y. and Yamaguchi,K.
TITLE NOVEL POLYPEPTIDE
JOURNAL Patent: JP.1988267292-A 1 04-NOV-1988;
COMMENT KYOWA HAKKO KOGYO CO LTD
OS Human
PN JP 1988267292-A/1
PD 04-NOV-1988
PF 23-DEC-1987 JP 1987326384
PR 23-DEC-1986 JP 86P 306799
PI KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI OKABE MASAMI, MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHITARU, YAMAGUCHI KAZUO
PC C12P21/02.C07K13/00.C12N1/00.C12N15/00//A61K37/02.A61K37/02.
PC A61K37/02.
PC (C12P21/02.C12N1-91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC *source: cell_line=Periferal macrophage;
FH Key Location/Qualifiers

FT mat_peptide 1..525 /product='mature peptide of hg-CSF'.
FT Location/Qualifiers
FEATURES
source
1..525
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 523; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCCCTGGCCCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
DB 1 ACCCCCCTGGCCCTCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
QY 61 GTGAGGAATCCAGGGGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
DB 61 GTGAGGAATCCAGGGGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
QY 121 CTGTGCCACCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGATCCCTGGGCTCCC 180
QY 181 CTGACGAGCTGCCCGAGCCAGCCCTGCTGAGCTGGCAGGCTCTTGAGCAACTCATAGC 240
DB 181 CTGACGAGCTGCCCGAGCCAGCCCTGCTGAGCTGGCAGGCTCTTGAGCAACTCATAGC 240
QY 241 GGCCTTTTCTTACCAGGGGCTCTGTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTTACCAGGGGCTCTGTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 300
QY 301 CCCACCTTGGACACTGAGCTGGAGCTGCGGACCTTTCAGCACCACCTATGCGAGCAG 360
DB 301 CCCACCTTGGACACTGAGCTGGAGCTGCGGACCTTTCAGCACCACCTATGCGAGCAG 360
QY 361 ATGGAAGAATCGGAATGGCCCTGCTGAGCCCTGAGGAGTCCATCCCGGCTTC 420
DB 361 ATGGAAGAATCGGAATGGCCCTGCTGAGCCCTGAGGAGTCCATCCCGGCTTC 420
QY 421 GCCTCTGCTTTCAGCGCGGGAGGAGGCTCTAGTTGCTCTCCATCTGAGAGCTTC 480
DB 421 GCCTCTGCTTTCAGCGCGGGAGGAGGCTCTAGTTGCTCTCCATCTGAGAGCTTC 480
QY 481 CTGGAGGTGCTGATCCCGGCTTCTACGCCACCTTGCCAGCCCT 523
DB 481 CTGGAGGTGCTGATCCCGGCTTCTACGCCACCTTGCCAGCCCT 523

RESULT 4
E02573 525 bp RNA linear PAT 29-SEP-1997
LOCUS
DEFINITION DNA encoding human colony-stimulating factor (hg-CSF).
ACCESSION E02573
VERSION E02573.1 GI:2170803
KEYWORDS JP 199027075-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Sasaki.K., Nishi.T., Yasumura.S., Sato.M. and Itou,S.
TITLE NEW POLYPEPTIDE
JOURNAL Patent: JP 199027075-A 1 10-SEP-1990;
KYOWA HAKKO KOGYO CO LTD
CS Homo sapiens (human)
PN JP 199027075-A/1
PD 10-SEP-1990
PF 28-SEP-1989 JP 1989253097
PI 29-SEP-1988 JP 88P 245705
PR SASAKI KATSUTOSHI, NISHI TATSUYA, YASUMURA SHIGEYOSHI, PI
SATO MORIYUKI,

PI ITOU SEIGA
PC C12N9/72.C07K13/00.C07K15/14.C12N1/21.C12N5/10.C12N9/64.PC
C12N15/27,
PC C12N15/58.C12N15/70.C12N15/85.C12P21/02.C12P21/02.(C12N1/21,
C12R1/19),
PC (C12P21/02.C12R1/19).(C12P21/02.C12R1/91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell type=lymphoblast LukII;
CC *source: clone=pCSF1-2;
FH Key Location/Qualifiers
FH mat_peptide 1..525 /product='human colony-stimulating FT
FT factor (hg-CSF)'.
FEATURES
source
1..525
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 523; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCCCTGGCCCTCCAGCTTCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
DB 1 ACCCCCCTGGCCCTCCAGCTTCCTGCCCCAGAGCTTCCTGCTCAAGTGTAGAGCAA 60
QY 61 GTGAGGAATCCAGGGGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
DB 61 GTGAGGAATCCAGGGGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
QY 121 CTGTGCCACCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGATCCCTGGGCTCCC 180
DB 121 CTGTGCCACCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGATCCCTGGGCTCCC 180
QY 181 CTGAGCAGCTGCCCGAGCCAGCCCTGCTGAGCTGGCAGGCTCTTGAGCAACTCATAGC 240
DB 181 CTGAGCAGCTGCCCGAGCCAGCCCTGCTGAGCTGGCAGGCTCTTGAGCAACTCATAGC 240
QY 241 GGCCTTTTCTTACCAGGGGCTCTGTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 300
DB 241 GGCCTTTTCTTACCAGGGGCTCTGTGAGGCCCTTGGAGGATCTCCCGAGTTGGGT 300
QY 301 CCCACCTTGGACACTGAGCTGGAGCTGCGGACCTTTCAGCACCACCTATGCGAGCAG 360
DB 301 CCCACCTTGGACACTGAGCTGGAGCTGCGGACCTTTCAGCACCACCTATGCGAGCAG 360
QY 361 ATGGAAGAATCGGAATGGCCCTGCTGAGCCCTGAGGAGTCCATCCCGGCTTC 420
DB 361 ATGGAAGAATCGGAATGGCCCTGCTGAGCCCTGAGGAGTCCATCCCGGCTTC 420
QY 421 GCCTCTGCTTTCAGCGCGGGAGGAGGCTCTAGTTGCTCTCCATCTGAGAGCTTC 480
DB 421 GCCTCTGCTTTCAGCGCGGGAGGAGGCTCTAGTTGCTCTCCATCTGAGAGCTTC 480
QY 481 CTGGAGGTGCTGATCCCGGCTTCTACGCCACCTTGCCAGCCCT 523
DB 481 CTGGAGGTGCTGATCCCGGCTTCTACGCCACCTTGCCAGCCCT 523
RESULT 5
E07164 525 bp RNA linear PAT 29-SEP-1997
LOCUS
DEFINITION cDNA encoding human G-CSF.
ACCESSION E07164
VERSION E07164.1 GI:2175311
KEYWORDS JP 1994092994-A/1.
SOURCE Homo sapiens (human)

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Kuga,T., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M.,
Itou,S., Yamazaki,M., Yokoo,Y. and Yamaguchi,K.
TITLE NEW POLYPEPTIDE
JOURNAL Patent: JP 1994092994-A 1 05-APR-1994;
KYOWA HAKKO KOGYO CO LTD
OS Homo sapiens (human)
PN 1994092994-A/1
PD 05-APR-1994
PF 23-DEC-1987 JP 1992214376
PI 23-DEC-1986 JP 86P 306799
PR KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
OKABE MASAMI
PI MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
FI YAMAGUCHI KAZUO
PC C07K13/00,A61K37/02,C12N1/21,C12N15/27,C12P21/02,(C12N1/21,PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical; No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..525
FT /organism='Homo sapiens'
FT /cell_type='macrophage'
FT /clone='pCSF1-2'
FT CDS 1..525
FT /product='human G-CSF'.
FT Location/Qualifiers
FT source 1..525
FT /organism='Homo sapiens'
FT /mol_type='genomic RNA'
FT /db_xref='taxon:9606'

FEATURES
source
1..525
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 100.0%; Score 523; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTCCAGAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
DB 1 ACCCCCTGGGCGCTCCAGAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAAG 120
QY 121 CTGTGCGACCCGAGAGAGCTGTGTGTCTCGGACACTCTCTGGGATATCCCTGGGCTCCC 180
DB 121 CTGTGCGACCCGAGAGAGCTGTGTGTCTCGGACACTCTCTGGGATATCCCTGGGCTCCC 180
QY 181 CTGAGCAGCTGCCCGAGCAGCCCTGTGAGCTGGCAGGCTGTCTGAGCAACTCCATAGC 240
DB 181 CTGAGCAGCTGCCCGAGCAGCCCTGTGAGCTGGCAGGCTGTCTGAGCAACTCCATAGC 240
QY 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTTGAAGAGGATCTCCCGGAGTTGGGT 300
DB 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTTGAAGAGGATCTCCCGGAGTTGGGT 300
QY 301 CCCACCTTGGACACACTGACGTGACGTCGCGGACTTTGCCACCACTCTGGCAGCAG 360
DB 301 CCCACCTTGGACACACTGACGTGACGTCGCGGACTTTGCCACCACTCTGGCAGCAG 360
QY 361 ATGGAAGAACTGGGAATGGCCCTTGCCTTGCAGCCCAACCCAGGCTGCCCGCCTTC 420
DB 361 ATGGAAGAACTGGGAATGGCCCTTGCCTTGCAGCCCAACCCAGGCTGCCCGCCTTC 420
QY 421 GCCTCTGCTTTCCAGCGCGGCGAGGAGGGGTCTCTAGTTGCTCCCATCTGCAGAGCTTC 480
DB 421 GCCTCTGCTTTCCAGCGCGGCGAGGAGGGGTCTCTAGTTGCTCCCATCTGCAGAGCTTC 480

Db 421 GCCTCTGCTTTCCAGCGCGGCGAGGAGGGGTCTCTAGTTGCTCCCATCTGCAGAGCTTC 480
Qy 481 CTGAGAGTGTCTACCGCGGTCTTACGCCACCTTGCCAGCCCT 523
Db 481 CTGAGAGTGTCTACCGCGGTCTTACGCCACCTTGCCAGCCCT 523

RESULT 6
E09431 525 bp RNA linear PAT 29-SEP-1997
LOCUS E09431
DEFINITION cDNA encoding hG-CSF.
ACCESSION E09431
VERSION E09431.1 GI:22026058
KEYWORDS JP 1995149798-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Kuga,T., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M.,
Itou,S., Yamazaki,M., Yokoo,Y. and Yamaguchi,K.
TITLE NEW POLYPEPTIDE
JOURNAL Patent: JP 1995149798-A 1 13-JUN-1995;
KYOWA HAKKO KOGYO CO LTD
OS Homo sapiens (human)
PN 1995149798-A/1
PD 13-JUN-1995
PF 08-AUG-1994 JP 1994185787
PR 23-DEC-1986 JP 86P 306799
PI KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
OKABE MASAMI, MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
FI MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
FI YAMAGUCHI KAZUO
PC C07K14/535,C12N1/21,C12N15/09,C12P21/02,A61K38/00,(C12N1/21,PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..525
FT /organism='Homo sapiens'
FT /mol_type='genomic RNA'
FT /db_xref='taxon:9606'

FEATURES
source
1..525
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 100.0%; Score 523; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGGCGCTCCAGAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
DB 1 ACCCCCTGGGCGCTCCAGAGCTCCCTGCCCCAGAGCTTCTCTCAAGTGCTTAGAGCAA 60
QY 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAAG 120
DB 61 GTGAGGAAGATCCAGGGCGATGGCGAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAAG 120
QY 121 CTGTGCGACCCGAGAGAGCTGTGTGTCTCGGACACTCTCTGGGATATCCCTGGGCTCCC 180
DB 121 CTGTGCGACCCGAGAGAGCTGTGTGTCTCGGACACTCTCTGGGATATCCCTGGGCTCCC 180
QY 181 CTGAGCAGCTGCCCGAGCAGCCCTGTGAGCTGGCAGGCTGTCTGAGCAACTCCATAGC 240
DB 181 CTGAGCAGCTGCCCGAGCAGCCCTGTGAGCTGGCAGGCTGTCTGAGCAACTCCATAGC 240
QY 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTTGAAGAGGATCTCCCGGAGTTGGGT 300
DB 241 GGCCTTTTCTCTACAGGGGTCTCTGAGGCCCTTGAAGAGGATCTCCCGGAGTTGGGT 300
```

QY 301 CCCACCTTGGACACACTGACGTGGACGTGCGCCGACTTTGCCACCAACATCTGCCAGCAG 360
 Db 301 CCCACCTTGGACACACTGACGTGGACGTGCGCCGACTTTGCCACCAACATCTGCCAGCAG 360
 QY 361 ATGGAAGAAGCTGGAAATGGCCCTGCGCTGAGCCACCCAGGGTGCATGCGGCGCTTC 420
 Db 361 ATGGAAGAAGCTGGAAATGGCCCTGCGCTGAGCCACCCAGGGTGCATGCGGCGCTTC 420
 QY 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGGTCTCTAGTTGCTCTCCCATCTGACAGAGCTTC 480
 Db 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGGTCTCTAGTTGCTCTCCCATCTGACAGAGCTTC 480
 QY 481 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCAGCCCT 523
 Db 481 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCAGCCCT 523

RESULT 7
 E15131
 LOCUS Human mRNA for granulocyte-colony stimulating factor.
 DEFINITION
 E15131
 ACCESSION
 E15131.1 GI:5709814
 VERSION
 JP 1998052281-A/1.
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Kuga,T., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M.,
 Itou,S., Yamazaki,M., Yokoo,Y., and Yamaguchi,K.
 NEW POLYPEPTIDE
 Patent: JP 1998052281-A 1 24-FEB-1998;
 KYOWA HAKKO KOGYO CO LTD
 OS Homo sapiens (human)
 PN JP 1998052281-A/1
 PD 24-FEB-1998
 PF 23-DEC-1987 JP 86P 306799
 PR 23-DEC-1987 JP 86P 306799
 PI KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
 OKABE MASAMI,
 PI MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
 PI YAMAGUCHI KAZUO
 PC C12N15/09,A61K38/00,C07K14/535,C12N1/21,C12P21/02,(C12P21/02,
 PC C12R1:19);
 CC strandedness: Double;
 CC topology: linear;
 FH key Location/Qualifiers

FT source 1..525
 /organism='Homo sapiens'
 FT mat_peptide 1..522
 /cell_type='peripheral blood macrophage' FT
 FT /product='G-CSF'.
 FEATURES
 source
 1..525
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

ORIGIN
 Query Match 100.0%; Score 523; DB 6; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.5e-86;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
 Db 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
 QY 61 GTGAGGAAGATCCAGGGCGATGGCGGAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
 Db 61 GTGAGGAAGATCCAGGGCGATGGCGGAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120

QY 121 CTGTGCCACCCGAGAGAGCTGGTGTCTGCGACACTCTCTGTGGGATCCCTGGGCTCC 180
 Db 121 CTGTGCCACCCGAGAGAGCTGGTGTCTGCGACACTCTCTGTGGGATCCCTGGGCTCC 180
 QY 181 CTGAGCAGCTGCCCGAGCCGCTGAGCTGGCAGGCTGTTGAGCCAACTCCATAGC 240
 Db 181 CTGAGCAGCTGCCCGAGCCGCTGAGCTGGCAGGCTGTTGAGCCAACTCCATAGC 240
 QY 241 GGCCTTTTCTCTACACAGGGGCTCCTGACGGCCCTGGAAGGATCTCCCCCGAGTTGGGT 300
 Db 241 GGCCTTTTCTCTACACAGGGGCTCCTGACGGCCCTGGAAGGATCTCCCCCGAGTTGGGT 300
 QY 301 CCCACCTTGGACACACTGACGTGGACGTCGCGAGCTTTGCCACCAACATCTGGCAGCAG 360
 Db 301 CCCACCTTGGACACACTGACGTGGACGTCGCGAGCTTTGCCACCAACATCTGGCAGCAG 360
 QY 361 ATGGAAGAAGCTGGAAATGGCCCTGCGCTGAGCCACCCAGGGTGCATGCGGCGCTTC 420
 Db 361 ATGGAAGAAGCTGGAAATGGCCCTGCGCTGAGCCACCCAGGGTGCATGCGGCGCTTC 420
 QY 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGGTCTCTAGTTGCTCTCCCATCTGACAGAGCTTC 480
 Db 421 GCCTCTGCTTTCCAGCGCCGGGAGGAGGGTCTCTAGTTGCTCTCCCATCTGACAGAGCTTC 480
 QY 481 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCAGCCCT 523
 Db 481 CTGGAGGTGCTGTAACCGGCTTCTAGCCACCTTGCAGCCCT 523

RESULT 8
 E171150
 LOCUS 171150 525 bp DNA linear PAT 03-APR-1998
 DEFINITION
 Sequence 1 from patent US 5681720.
 ACCESSION
 E171150
 VERSION
 171150.1 GI:3007285
 KEYWORDS
 SOURCE
 Unknown.
 ORGANISM
 Unclassified.
 REFERENCE
 1 (bases 1 to 525)
 AUTHORS
 Kuga,T., Miyaji,H., Sato,M., Okabe,M., Morimoto,M., Itoh,S.,
 Yamazaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.
 TITLE
 DNA encoding human granulocyte colony stimulating factor plasmids
 and host cells comprising same, and methods of expressing the
 encoded polypeptide
 JOURNAL
 Patent: US 5681720-A 1 28-OCT-1997;
 FEATURES
 source
 1..525
 Location/Qualifiers
 /organism='unknown'
 /mol_type='unassigned DNA'

ORIGIN
 Query Match 100.0%; Score 523; DB 6; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.5e-86;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
 Db 1 ACCCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCTGCTCAAGTCTTAGAGCAA 60
 QY 61 GTGAGGAAGATCCAGGGCGATGGCGGAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
 Db 61 GTGAGGAAGATCCAGGGCGATGGCGGAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
 QY 121 CTGTGCCACCCGAGAGAGCTGGTGTCTGCGACACTCTCTGGGATCCCTGGGCTCC 180
 Db 121 CTGTGCCACCCGAGAGAGCTGGTGTCTGCGACACTCTCTGGGATCCCTGGGCTCC 180
 QY 181 CTGAGCAGCTGCCCGAGCCGCTGAGCTGGCAGGCTGTTGAGCCAACTCCATAGC 240
 Db 181 CTGAGCAGCTGCCCGAGCCGCTGAGCTGGCAGGCTGTTGAGCCAACTCCATAGC 240


```

RESULT 11
HUMGCSF
LOCUS Human granulocyte colony stimulating factor mRNA, complete cds.
DEFINITION M17706
ACCESSION M17706.1 GI:183040
VERSION granulocyte colony stimulating factor.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 660)
AUTHORS Devlin,J.J., Devlin,P.E., Myambo,K., Lilly,M.B., Rado,T.A. and Warren,M.K.
TITLE Expression of granulocyte colony-stimulating factor by human cell lines
JOURNAL J. Leukoc. Biol. 41 (4), 302-306 (1987)
MEDLINE 87156936
PUBMED 3494801
COMMENT Original source text: Human M1A PaCa-2 cell line, cDNA to mRNA, (library of Kawasaki et al.), clone pP12.
FEATURES
source
1..660
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
43..657
/note="granulocyte colony stimulating factor precursor"
/codon_start=1
/protein_id="AAA35882.1"
/db_xref="GI:183041"
/translation="MAGPATQSPMKLMALQLLVHSLVTVQVETPLGPASSLPQSLF
LKLEQVRKICGDGAALQKLCATYKCHPELVLLGHSLGIPWAPLSSCFPSQALQLA
KCLQSHGLFLYQGLQALGEGISPELGTDLTLDLVADFPATTIQQWMEELGMAPAL
OPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP"
43..132
sig_peptide
/note="granulocyte colony stimulating factor signal peptide"
43..132
mat_peptide
133..654
/product="granulocyte colony-stimulating factor"
ORIGIN Unreported.
Query Match 100.0%; Score 523; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.4e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCCTGGGCTTCCAGGGGCTCCCTGCGAGCTTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 60
DB 133 ACCCCCTGGGCTTCCAGCTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 192
QY 61 GTGAGGAAGATCCAGGGGCTGCGAGCGCTCCAGAGAGCTGTGTGCCACCTACAAG 120
DB 193 GTGAGGAAGATCCAGGGGCTGCGAGCGCTCCAGAGAGCTGTGTGCCACCTACAAG 252
QY 121 CTGTGCCACCCCGAGGAGCTGTGTCTCGGACACTCTCTGGGCACTCCCTGGGCTCCC 180
DB 253 CTGTGCCACCCCGAGGAGCTGTGTCTCGGACACTCTCTGGGCACTCCCTGGGCTCCC 312
QY 181 CTGAGCAGCTGCCCGACGAGCGCTCCAGCTGCGAGCTGTGTGCCAATCTCCATAGC 240
DB 313 CTGAGCAGCTGCCCGACGAGCGCTCCAGCTGCGAGCTGTGTGCCAATCTCCATAGC 372
QY 241 GGCCTTTTCTCTACCAAGGGGCTCCCTGCGAGCGCTCCGAGGATCTCCCGGAGTTGGGT 300
DB 373 GGCCTTTTCTCTACCAAGGGGCTCCCTGCGAGCGCTCCGAGGATCTCCCGGAGTTGGGT 432
QY 301 CCCACCTTGGACACACTGAGCTGGAGCTGCGGACATTTTGGCCACCACTCTGGCAGCAG 360
DB 433 CCCACCTTGGACACACTGAGCTGGAGCTGCGGACATTTTGGCCACCACTCTGGCAGCAG 492
QY 361 ATGAAGAAGCTGGGAATGGCCCTTCCCTGCGAGCGCTCCAGCCACCCAGAGTGCCATGCGCGCTTC 420
DB 493 ATGAAGAAGCTGGGAATGGCCCTTCCCTGCGAGCGCTCCAGCCACCCAGAGTGCCATGCGCGCTTC 552

```

```

QY 421 GCCTCTGCTTTCCAGGCGCCGCGAGAGGGGTCTAGTTCCTCCATCTGCAGAGCTTC 480
DB 553 GCCTCTGCTTTCCAGGCGCCGCGAGAGGGGTCTAGTTCCTCCATCTGCAGAGCTTC 612
QY 481 CTGAGAGGTGCTACCGCGCTTCTACGCCACCTTGCAGGCGCT 523
DB 613 CTGAGAGGTGCTACCGCGCTTCTACGCCACCTTGCAGGCGCT 655

RESULT 12
HSGCSFRI
LOCUS Human mRNA for granulocyte colony-stimulating factor (G-CSF)
DEFINITION (pBRV-2).
ACCESSION X03655
VERSION X03655.1 GI:31693
KEYWORDS colony stimulating factor; signal peptide.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1498)
AUTHORS Nagata,S., Tsuchiya,M., Asano,S., Yamamoto,O., Hirata,Y., Kubota,N., Oheda,M., Nomura,H. and Yamazaki,T.
TITLE The chromosomal gene structure and two mRNAs for human granulocyte colony-stimulating factor
JOURNAL EMBO J. 5 (3), 575-581 (1986)
MEDLINE 86220137
PUBMED 2423327
COMMENT Data kindly reviewed (19-JUN-1986) by S. Nagata.
FEATURES
source
1..1498
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
31..1645
/codon_start=1
/product="G-CSF protein"
/protein_id="CAA27290.1"
/db_xref="GI:732764"
/db_xref="GOA:P09919"
/db_xref="SWISS-PROT:P09919"
/translation="MAGPATQSPMKLMALQLLVHSLVTVQVETPLGPASSLPQSLF
LKLEQVRKICGDGAALQKLCATYKCHPELVLLGHSLGIPWAPLSSCFPSQALQLA
KCLQSHGLFLYQGLQALGEGISPELGTDLTLDLVADFPATTIQQWMEELGMAPAL
OPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP"
31..120
sig_peptide
/note="signal peptide (aa -30 to -1)"
121..1642
mat_peptide
/product="mature G-CSF protein (aa 1-174)"
1481..1486
misc_feature
/note="polyadenylation signal"
1498
polyA_site
/note="polyadenylation site"
ORIGIN

Query Match 100.0%; Score 523; DB 9; Length 1498;
Best Local Similarity 100.0%; Pred. No. 2.1e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCCTGGGCTTCCAGGGGCTCCCTGCGAGCTTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 60
DB 121 ACCCCCTGGGCTTCCAGCTTCCCTGCCAGAGCTTCTCTCAAGTCTTAGAGCAA 180
QY 61 GTGAGGAAGATCCAGGGGCTGCGAGCGCTCCAGAGAGCTGTGTGCCACCTACAAG 120
DB 181 GTGAGGAAGATCCAGGGGCTGCGAGCGCTCCAGAGAGCTGTGTGCCACCTACAAG 240
QY 121 CTGTGCCACCCCGAGGAGCTGTGTCTCGGACACTCTCTGGGCACTCCCTGGGCTCCC 180
DB 241 CTGTGCCACCCCGAGGAGCTGTGTCTCGGACACTCTCTGGGCACTCCCTGGGCTCCC 300

```


QY 121 CTGTGCCACCCGAGAGCTGTGTCTGTGAGACACTCTCTGGGGCATCCCTGGGCTCCC 180
Db 253 CTGTGCCACCCGAGAGCTGTGTCTGTGAGACACTCTCTGGGGCATCCCTGGGCTCCC 312
QY 181 CTGAGCAGTGCCCGAGCAGCCCTGCAGCTGGCAGGCTGTCTGAGCAACTCCATAGC 240
Db 313 CTGAGCAGTGCCCGAGCAGCCCTGCAGCTGGCAGGCTGTCTGAGCAACTCCATAGC 372
QY 241 GGCCTTTTCTCTACACAGGGGTCTCTGAGGCCCTGGGAAGGATCTCCCGAGTTGGT 300
Db 373 GGCCTTTTCTCTACACAGGGGTCTCTGAGGCCCTGGGAAGGATCTCCCGAGTTGGT 432
QY 301 CCCACTTTGGACACACTGCAGCTGCAGCTGCAGGCTGTGAGCAACTCCATAGC 360
Db 433 CCCACTTTGGACACACTGCAGCTGCAGGCTGTGAGCAACTCCATAGC 492
QY 361 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCACCCAGGGTGCCATCCCGGCTTC 420
Db 493 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCACCCAGGGTGCCATCCCGGCTTC 552
QY 421 GCCTCTGTCTTCCAGCGCGGCGAGGAGGCTCTAGTTGCTTCCATCTGCAGAGCTTC 480
Db 553 GCCTCTGTCTTCCAGCGCGGCGAGGAGGCTCTAGTTGCTTCCATCTGCAGAGCTTC 612
QY 481 CTGAGGTTGTCTACCGGCTTCTACGCCACCTTGCCAGCCCT 523
Db 613 CTGAGGTTGTCTACCGGCTTCTACGCCACCTTGCCAGCCCT 655

RESULT 15

LOCUS I08669 1525 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent WO 8801297.
ACCESSION I08669
VERSION I08669.1 GI:588622
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1525)
AUTHORS Devlin, J.J., Kawasaki, E.S. and Warren, M.K.
JOURNAL Patent: WO 8801297-A 1 25-FEB-1998;
FEATURES
source location/Qualifiers
1..1525
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 1525;
Best Local Similarity 100.0%; Pred. No. 2.1e-86;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCCTGGGCTTCCAGCTCCCTGCCCGAGGCTTCTGCTCAAGTGCTTAGAGCAA 60
Db 133 ACCCCCTGGGCTTCCAGCTCCCTGCCCGAGGCTTCTGCTCAAGTGCTTAGAGCAA 192
QY 61 GTGAGGAAGATCCAGGCGATGGCGAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
Db 193 GTGAGGAAGATCCAGGCGATGGCGAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 252
QY 121 CTGTGCCACCCGAGGAGCTGTGTCTGTGAGCAACTCTCTGGGCATCCCTGGGCTCCC 180
Db 253 CTGTGCCACCCGAGGAGCTGTGTCTGTGAGCAACTCTCTGGGCATCCCTGGGCTCCC 312
QY 181 CTGAGCAGTGCCCGAGCAGCCCTGCAGCTGGCAGGCTGTGAGCAACTCCATAGC 240
Db 313 CTGAGCAGTGCCCGAGCAGCCCTGCAGCTGGCAGGCTGTGAGCAACTCCATAGC 372
QY 241 GGCCTTTTCTCTACACAGGGGTCTCTGAGGCCCTGGGAAGGATCTCCCGAGTTGGT 300
Db 373 GGCCTTTTCTCTACACAGGGGTCTCTGAGGCCCTGGGAAGGATCTCCCGAGTTGGT 432

QY 301 CCCACTTTGGACACACTGCAGCTGGAGCTGGCGGACTTTTGGCCACCCATCTGGCAGCAG 360
Db 433 CCCACTTTGGACACACTGCAGCTGGAGCTGGCGGACTTTTGGCCACCCATCTGGCAGCAG 492
QY 361 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCACCCAGGGTGCCATCCCGGCTTC 420
Db 493 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCACCCAGGGTGCCATCCCGGCTTC 552
QY 421 GCCTCTGTCTTCCAGCGCGGCGAGGAGGCTCTAGTTGCTTCCATCTGCAGAGCTTC 480
Db 553 GCCTCTGTCTTCCAGCGCGGCGAGGAGGCTCTAGTTGCTTCCATCTGCAGAGCTTC 612
QY 481 CTGAGGTTGTCTACCGGCTTCTACGCCACCTTGCCAGCCCT 523
Db 613 CTGAGGTTGTCTACCGGCTTCTACGCCACCTTGCCAGCCCT 655

Search completed: October 9, 2004, 03:08:31
Job time : 2729.62 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 00:53:40 ; Search time 1111.24 seconds
(without alignments)
4837.123 Million cell updates/sec

Title: US-10-009-792c-26
Perfect score: 180
Sequence: 1 atgtttaagttaaaagaa.....tcctgctaagtgcttagag 180

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	52	28.9	346 14	CB705562
2	49	27.2	314 14	CB136760
3	49	27.2	554 14	CB126975
4	49	27.2	579 14	CB127794

5 49 27.2 12 BG548320
6 49 27.2 29 AY414901
7 49 27.2 29 CD013926
8 49 27.2 29 AY414900
9 49 27.2 789 14 CD013925
10 49 27.2 802 14 CA489740
11 49 27.2 817 12 BM009358
12 49 27.2 897 14 CD013924
13 49 27.2 906 14 CA487627
14 49 27.2 948 12 BI822673
15 49 27.2 983 12 BM557421
16 49 27.2 986 14 CA487516
17 49 27.2 990 12 BM423896
18 49 27.2 993 12 BM915836
19 49 27.2 1012 12 BM556479
20 49 27.2 1080 12 BM553432
21 49 27.2 1096 12 BM923410
22 49 27.2 1123 12 BM554035
23 49 27.2 1141 12 BM906188
24 49 27.2 1445 12 BM906367
25 47.4 26.3 368 12 BI961002
26 47.4 26.3 548 12 BI960812
27 47.4 26.3 570 12 BI961242
28 44.2 24.6 509 12 BM256261
29 44.2 24.6 513 10 BE480590
30 44.2 24.6 1375 12 BM554037
31 36.4 20.2 777 12 BG571954
32 34.6 19.2 888 13 BO716545
33 34.2 19.0 887 29 CNS020VH
34 33.8 18.6 754 29 CNS004TE
35 33.4 18.4 829 12 BM009247
36 33.2 18.4 675 28 CC100458
37 33 18.3 538 14 CA621905
38 33 18.3 1005 29 CG998971
39 33 18.3 1100 12 BI079593
40 32.8 18.2 854 29 CG674466
41 32.6 18.1 489 28 AQ721853
42 32.6 18.1 924 29 CNS047GV
43 32.4 18.0 1216 10 BF137044
44 32.2 17.9 454 13 BX565066
45 32.2 17.9 473 13 BX557098

ALIGNMENTS

RESULT 1
CB705562
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

CB705562
AMGNNUC:TRCX1-00003-C7-A ttrxl (10261) Rattus norvegicus cDNA clone
trcx1-00003-c7 5', mRNA sequence.
CB705562
CB705562.1 GI:29762710
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 346)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00003 row: c column: 7.
Location/Qualifiers
1..346
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"

CB705562 AMGNNUC.T
CB136760 K-EST0189
CB126975 K-EST0176
CB127794 K-EST0177

ORIGIN		/clone="trcx1-00003-c7" /tissue type="choroid plexus brain" /clone.lib="trcx1 (10261)" /note="Vector: pCAV; Site_1: Sali; Site_2: NotI; choroid plexus brain region"	
Query Match	28.9%; Score 52; DB 14; Length 346;		
Best Local Similarity	72.8%; Pred. No. 3.4e-05;		
Matches	67; Conservative 0; Mismatches 25; Indels 0; Gaps 0;		
ORIGIN			
QY	89 GCGCCACATCACCATACCATATCGAGGGAAGGACTCCGTTAGGTCACGAGCTCCC 148		
Db	28 GCGCCGAGCTCCAGCTCCCATGACCCAGCTAGAACCCCTGGGCGCTGCCAGTCCC 87		
QY	149 TGCCCCAGAGCTTCCTGCTCAAGTCTTAGAG 180		
Db	88 TGCCCCAGAGCTTCCTGCTCAAGTCTTAGAG 119		
RESULT 2			
LOCUS	CB136760	314 bp	mRNA
DEFINITION	K-BST0189338 L5HLK1 Homo sapiens cDNA clone L5HLK1-42-H10 5', mRNA		
ACCESSION	CB136760		
VERSION	CB136760.1	GI:29104242	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 314)		
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.		
TITLE		21C Frontier Korean EST Project 2001	
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kr.ibm.re.kr Plate: 42 row: H column: 10 High quality sequence stop: 314. Location/Qualifiers		
FEATURES		source	
1..314		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="L5HLK1-42-H10" /sex="M" /cell_line="HLK-1" /lab_host="Top10F" /clone.lib="L5HLK1" /note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	

Best Local Similarity 84.6%; Pred. No. 0.00034; Mismatches 0; Indels 10; Gaps 0;

QY 116 AGGAAGGACTCCGTTAGGTCACAGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCT 175
Db 121 AGGAAGCACCCTCGGCTCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCT 180

QY 176 TAGAG 180
Db 181 TAGAG 185

RESULT 4
LOCUS K-EST0177131 C1SNU17 Homo sapiens cDNA clone C1SNU17-10-C09 5',
DEFINITION mRNA sequence.

ACCESSION CB127794

VERSION CB127794.1

KEYWORDS GI:28090473

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Authors Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 579)

Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Ch.K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 10 row: C column: 09

High quality sequence stop: 579.

Location/Qualifiers

1..579

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="C1SNU17-10-C09"

/sex="F"

/tissue_type="uterine"

/cell_type="Epithelial"

/cell_line="SNU-17"

/lab_host="Top10F"

/clone_lib="C1SNU17"

/note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI;

Site 2: NotI; The poly (A) RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated

with tobacco acid pyrophosphatase (TAP). The dephosphorylated

intact mRNA was ligated with DNA-RNA linker including

EcoRI site by treatment of T4 RNA ligase and the first

strand cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

ORIGIN

Query Match 27.2%; Score 49; DB 14; Length 579;
Best Local Similarity 84.6%; Pred. No. 0.00035;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAAGGACTCCGTTAGGTCACAGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCT 175
Db 197 AGGAAGCACCCTCGGCTCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCT 256

QY 176 TAGAG 180
Db 257 TAGAG 261

RESULT 5

LOCUS BG548320

DEFINITION 602575289F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703159 5',

mRNA sequence.

ACCESSION BG548320

VERSION BG548320.1

KEYWORDS GI:13546985

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 598)

Authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Journal Contact: Robert Strausberg, Ph.D.

Comment Email: cgabs-r@mail.nih.gov

Tissue procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1541 row: b column: 24

High quality sequence stop: 597.

Location/Qualifiers

1..598

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4703159"

/lab_host="DH10B (Tl phage-resistant)"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:

SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctcgcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGCGCGCGCGCATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.2%; Score 49; DB 12; Length 598;
Best Local Similarity 84.6%; Pred. No. 0.00035;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAAGGACTCCGTTAGGTCACAGCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCT 175
Db 80 AGGAAGCACCCTCGGCTCCAGCTCCCTGCCAGAGCTTCTCTCAAGTGCT 139

QY 176 TAGAG 180
Db 140 TAGAG 144

RESULT 6

LOCUS AY414901

DEFINITION Pan troglodytes CSF3 gene, VIRTUAL TRANSCRIPT, partial sequence,

AY414901

608 bp DNA linear GSS 17-DEC-2003

```

ACCESSION      AV414901
VERSION        AV414901.1 GI:39770860
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1 (bases 1 to 608)
AUTHORS        Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
TITLE          Inferring nonneutral evolution from human-chimp-mouse orthologous
               gene trios
JOURNAL        Science 302 (5652), 1960-1963 (2003)
PUBMED         14671302
REFERENCE      2 (bases 1 to 608)
AUTHORS        Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
TITLE          Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
               Rockville, MD 20850, USA
COMMENT        This sequence was made by sequencing genomic exons and ordering
               them based on alignment.
FEATURES       Location/Qualifiers
               source             1..608
                                   /organism="Pan troglodytes"
                                   /mol_type="genomic DNA"
                                   /db_xref="taxon:9598"
               gene               <1..>608
                                   /gene="CSF3"
                                   /locus_tag="HCM5378"
ORIGIN
Query Match      27.2%; Score 49; DB 29; Length 608;
Best Local Similarity 84.6%; Pred. No. 0.00035;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAGGAGGACTCGGTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 175
Db 67 AGGAGCCACCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 126

QY 176 TAGAG 180
Db 127 TAGAG 131

RESULT 7
CD013926
LOCUS           CD013926 622 bp mRNA linear EST 21-OCT-2003
DEFINITION      90138855 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION       CD013926
VERSION         CD013926.1 GI:37777456
KEYWORDS        BST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 622)
AUTHORS        Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
               Au-Young,J. and Stuve,L.L.
TITLE          PCR isolation and cloning of novel splice variant mRNAs from known
               drug target genes
JOURNAL        Unpublished (2003)
COMMENT        Contact: Jin, P.
               Incyte Corporation
               3160 Porter Drive, Palo Alto, CA 94304, USA
               Tel: 650 621 8639
               Fax: 650 621 8965
               Email: pjin@incyte.com.

Genomic survey sequence.
ACCESSION      AV414901
VERSION        AV414901.1 GI:39770860
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1 (bases 1 to 608)
AUTHORS        Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
TITLE          Inferring nonneutral evolution from human-chimp-mouse orthologous
               gene trios
JOURNAL        Science 302 (5652), 1960-1963 (2003)
PUBMED         14671302
REFERENCE      2 (bases 1 to 608)
AUTHORS        Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
TITLE          Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
               Rockville, MD 20850, USA
COMMENT        This sequence was made by sequencing genomic exons and ordering
               them based on alignment.
FEATURES       Location/Qualifiers
               source             1..608
                                   /organism="Pan troglodytes"
                                   /mol_type="genomic DNA"
                                   /db_xref="taxon:9598"
               gene               <1..>608
                                   /gene="CSF3"
                                   /locus_tag="HCM5378"
ORIGIN
Query Match      27.2%; Score 49; DB 29; Length 608;
Best Local Similarity 84.6%; Pred. No. 0.00035;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAGGAGGACTCGGTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 175
Db 67 AGGAGCCACCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 126

QY 176 TAGAG 180
Db 127 TAGAG 131

RESULT 7
CD013926
LOCUS           CD013926 622 bp mRNA linear EST 21-OCT-2003
DEFINITION      90138855 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION       CD013926
VERSION         CD013926.1 GI:37777456
KEYWORDS        BST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 622)
AUTHORS        Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
               Au-Young,J. and Stuve,L.L.
TITLE          PCR isolation and cloning of novel splice variant mRNAs from known
               drug target genes
JOURNAL        Unpublished (2003)
COMMENT        Contact: Jin, P.
               Incyte Corporation
               3160 Porter Drive, Palo Alto, CA 94304, USA
               Tel: 650 621 8639
               Fax: 650 621 8965
               Email: pjin@incyte.com.

FEATURES       Location/Qualifiers
               source             1..622
                                   /organism="Homo sapiens"
                                   /mol_type="mRNA"
                                   /db_xref="taxon:9606"
                                   /clone_lib="Single Gene library"
                                   /notes="Vector: pDrive Cloning Vector; RT-PCR was performed
                                   using gene-specific primers flanking the open-reading
                                   frame. PCR products were subcloned into pDrive Cloning
                                   Vector and sequenced completely using M13 forward and
                                   reverse primers. Sequencing gaps were closed by
                                   re-sequencing using primers flanking the gapped areas."
ORIGIN
Query Match      27.2%; Score 49; DB 14; Length 622;
Best Local Similarity 84.6%; Pred. No. 0.00036;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAGGAGGACTCGGTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 175
Db 91 AGGAGGCCACCCCTGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 150

QY 176 TAGAG 180
Db 151 TAGAG 155

RESULT 8
AV414900
LOCUS           AV414900 624 bp DNA linear GSS 17-DEC-2003
DEFINITION      Homo sapiens CSF3 gene, VIRTUAL TRANSCRIPT, partial sequence,
               genomic survey sequence.
ACCESSION       AV414900
VERSION         AV414900.1 GI:39770859
KEYWORDS        GSS.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 624)
AUTHORS        Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
TITLE          Inferring nonneutral evolution from human-chimp-mouse orthologous
               gene trios
JOURNAL        Science 302 (5652), 1960-1963 (2003)
PUBMED         14671302
REFERENCE      2 (bases 1 to 624)
AUTHORS        Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
TITLE          Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
               Rockville, MD 20850, USA
COMMENT        This sequence was made by sequencing genomic exons and ordering
               them based on alignment.
FEATURES       Location/Qualifiers
               source             1..624
                                   /organism="Homo sapiens"
                                   /mol_type="genomic DNA"
                                   /db_xref="taxon:9606"
                                   <1..>624
                                   /gene="CSF3"
                                   /locus_tag="HCM5378"
ORIGIN
Query Match      27.2%; Score 49; DB 29; Length 624;
Best Local Similarity 84.6%; Pred. No. 0.00036;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAGGAGGACTCGGTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGCT 175

```

```

Db      83 AGGAAGCCACCCCTGGCCCTGCCAGCTCCCTGCCGCCAGAGCTTCTGCTCAAGTGCT 142
QY      176 TAGAG 180
Db      143 TAGAG 147

RESULT 9
CD013925 789 bp mRNA linear EST 21-OCT-2003
LOCUS 90138939 Single gene library Homo sapiens cDNA, mRNA sequence.
DEFINITION CD013925
ACCESSION CD013925
VERSION CD013925.1 GI:37777455
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 789)
AUTHORS Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Young, J. and Stuve, L.L.
TITLE PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
JOURNAL Unpublished (2003)
COMMENT Contact: Jin, P.
Incyte Corporation
3150 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pj@incyte.com.

FEATURES
source
1..789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN
Query Match 27.2%; Score 49; DB 14; Length 789;
Best Local Similarity 84.6%; Pred. No. 0.00039;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAAGGACTCCGTTAGTCCAGCCAGCTCCCTGCCGCCAGAGCTTCTGCTCAAGTGCT 175
Db 267 AGGAAGCCACCCCTGGCCCTGCCAGCTCCCTGCCGCCAGAGCTTCTGCTCAAGTGCT 325

QY 176 TAGAG 180
Db 327 TAGAG 331

RESULT 10
CD489740 802 bp mRNA linear EST 14-NOV-2002
LOCUS AGENCOURT_10810586 MAPcL Homo sapiens cDNA clone IMAGE:6722223 5',
DEFINITION mRNA sequence.
ACCESSION CA489740
VERSION CA489740.1 GI:24952531
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 802)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

```

```

JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14284 row: j column: 15
High quality sequence stop: 249.

FEATURES
source
1..802
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6722223"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
HRT-1, HME1, LNCaP"
/lab_host="EMDH108"
/clone_lib="MAPcL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dt. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN
Query Match 27.2%; Score 49; DB 14; Length 802;
Best Local Similarity 84.6%; Pred. No. 0.00039;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGAAGGACTCCGTTAGTCCAGCCAGCTCCCTGCCGCCAGAGCTTCTGCTCAAGTGCT 175
Db 107 AGGAAGCCACCCCTGGCCCTGCCAGCTCCCTGCCGCCAGAGCTTCTGCTCAAGTGCT 166

QY 176 TAGAG 180
Db 167 TAGAG 171

RESULT 11
BM009358 817 bp mRNA linear EST 30-OCT-2001
LOCUS 603629823F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443757 5',
DEFINITION mRNA sequence.
ACCESSION BM009358
VERSION BM009358.1 GI:16523712
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1921 row: m column: 06
High quality sequence stop: 745.

FEATURES
Location/Qualifiers

```

```

source
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5443757"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/Note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCGACGAC(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 27.2%; Score 49; DB 12; Length 817;
Best Local Similarity 84.6%; Pred. No. 0.00039;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGGAAGGACTCGTTAGTCCAGCCAGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 175
Db 270 AGGAAGCCACCCCGCTGGCGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 329

QY 176 TAGAG 180
Db 330 TAGAG 334

RESULT 12
CD013924 897 bp mRNA linear EST 21-OCT-2003
LOCUS
DEFINITION
Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION
CD013924.1 GI:37777454
VERSION
EST.
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Yang, J. and Stuve, L.L.
PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
Unpublished (2003)
JOURNAL
Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

FEATURES
Location/Qualifiers
1..897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/Note="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN
Query Match 27.2%; Score 49; DB 14; Length 897;
Best Local Similarity 84.6%; Pred. No. 0.00041;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGGAAGGACTCGTTAGTCCAGCCAGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 175
Db 270 AGGAAGCCACCCCGCTGGCGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 329

source
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5443757"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/Note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCGACGAC(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 27.2%; Score 49; DB 12; Length 817;
Best Local Similarity 84.6%; Pred. No. 0.00039;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGGAAGGACTCGTTAGTCCAGCCAGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 175
Db 270 AGGAAGCCACCCCGCTGGCGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 329

QY 176 TAGAG 180
Db 330 TAGAG 334

RESULT 13
CD013924 897 bp mRNA linear EST 14-NOV-2002
LOCUS
DEFINITION
Single gene library Homo sapiens cDNA clone IMAGE:6719127 5',
mRNA sequence.
ACCESSION
CD013924.1 GI:24947489
VERSION
EST.
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 906)
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14276 row: 1 column: 15
High quality sequence stop: 712.

FEATURES
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719127"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HMEL, LNCap"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/Note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN
Query Match 27.2%; Score 49; DB 14; Length 906;
Best Local Similarity 84.6%; Pred. No. 0.00041;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 116 AGGGAAGGACTCGTTAGTCCAGCCAGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 175
Db 72 AGGAAGCCACCCCGCTGGCGCTCCCTGCCCGAGCTTCTGCTCAAGTGCT 131

QY 176 TAGAG 180
Db 132 TAGAG 136

RESULT 14
BI822673 948 bp mRNA linear EST 04-OCT-2001
LOCUS
DEFINITION
NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5177209 5',
mRNA sequence.

```


ACCESSION BI822673
VERSION BI822673.1 GI:15934223
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 948)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM1441 row: k column: 02
High quality sequence stop: 845.
Location/Qualifiers
1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5177209"
/lab_host="DH108"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

FEATURES
source
1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5177209"
/lab_host="DH108"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 27.2%; Score 49; DB 12; Length 948;
Best Local Similarity 84.6%; Pred. No. 0.00042;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 116 AGGGAAGACTCCGTAGTCCAGCCAGCTCCCTCCGCCAGAGCTTCCTGCTCAAGTGCT 175
Db |||||
287 AGGAAGCCACCCCTGGGCGCTGCCAGTCCCTCCGCCAGAGCTTCCTGCTCAAGTGCT 346
QY 176 TAGAG 180
Db |||||
347 TAGAG 351

RESULT 15
BM557421
LOCUS BM557421 983 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6578800 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5466747
5' mRNA sequence.
ACCESSION BM557421
VERSION BM557421.1 GI:18799394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 983)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCMI967 row: k column: 04
High quality sequence stop: 593.
Location/Qualifiers
1..983
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5466747"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: Skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 27.2%; Score 49; DB 12; Length 983;
Best Local Similarity 84.6%; Pred. No. 0.00042;
Matches 55; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 116 AGGAAGGACTCCGTAGTCCAGCCAGCTCCCTCCGCCAGAGCTTCCTGCTCAAGTGCT 175
Db |||||
137 AGGAAGCCACCCCTGGGCGCTGCCAGTCCCTCCGCCAGAGCTTCCTGCTCAAGTGCT 196
QY 176 TAGAG 180
Db |||||
197 TAGAG 201

Search completed: October 9, 2004, 04:22:29
Job time : 1114.24 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2004, 03:08:44 ; Search time 154.651 Seconds
(without alignments)
5900.506 Million cell updates/sec

Title: US-10-009-792C-26

Perfect score: 180

Sequence: 1 atgtttaagtttaaaagaa.....tctgtcctaagtgcttagag 180

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues 6681306

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	180	100.0	180	15	US-10-009-792A-26
2	86	47.8	135	15	US-10-009-792A-24
3	79	43.9	645	15	US-10-237-386-10
4	72.8	40.4	657	15	US-10-237-386-11
5	50.6	28.1	546	15	US-10-083-446-177
6	50.6	28.1	546	15	US-10-083-446-178
7	50.6	28.1	906	15	US-10-083-446-53
8	50.6	28.1	921	15	US-10-083-446-72
9	50.6	28.1	921	15	US-10-083-446-75
10	50.6	28.1	921	15	US-10-083-446-78
11	50.6	28.1	921	15	US-10-083-446-84
12	50.6	28.1	966	15	US-10-083-446-68
13	50.6	28.1	966	15	US-10-083-446-70
14	50.6	28.1	966	15	US-10-083-446-71

15	50.6	28.1	966	15	US-10-083-446-73	Sequence 73, Appl
16	50.6	28.1	966	15	US-10-083-446-77	Sequence 77, Appl
17	50.6	28.1	966	15	US-10-083-446-79	Sequence 79, Appl
18	50.6	28.1	1017	15	US-10-083-446-67	Sequence 67, Appl
19	50.6	28.1	1047	15	US-10-083-446-74	Sequence 74, Appl
20	50.6	28.1	1047	15	US-10-083-446-76	Sequence 76, Appl
21	49	27.2	507	15	US-10-009-792A-17	Sequence 17, Appl
22	49	27.2	531	17	US-10-695-584A-17	Sequence 289, Appl
23	49	27.2	531	17	US-10-695-584A-290	Sequence 290, Appl
24	49	27.2	531	17	US-10-695-584A-292	Sequence 292, Appl
25	49	27.2	531	17	US-10-695-584A-293	Sequence 293, Appl
26	49	27.2	531	17	US-10-695-584A-295	Sequence 295, Appl
27	49	27.2	531	17	US-10-695-584A-296	Sequence 296, Appl
28	49	27.2	531	17	US-10-695-584A-297	Sequence 297, Appl
29	49	27.2	531	17	US-10-695-584A-298	Sequence 298, Appl
30	49	27.2	531	17	US-10-695-584A-299	Sequence 299, Appl
31	49	27.2	531	17	US-10-695-584A-313	Sequence 313, Appl
32	49	27.2	635	15	US-10-009-792A-18	Sequence 18, Appl
33	49	27.2	630	13	US-10-609-346-17	Sequence 17, Appl
34	49	27.2	975	17	US-10-695-584A-263	Sequence 263, Appl
35	49	27.2	975	17	US-10-695-584A-264	Sequence 264, Appl
36	49	27.2	975	17	US-10-695-584A-265	Sequence 265, Appl
37	49	27.2	975	17	US-10-695-584A-266	Sequence 266, Appl
38	49	27.2	975	17	US-10-695-584A-267	Sequence 267, Appl
39	49	27.2	975	17	US-10-695-584A-268	Sequence 268, Appl
40	49	27.2	975	17	US-10-695-584A-269	Sequence 269, Appl
41	49	27.2	975	17	US-10-695-584A-270	Sequence 270, Appl
42	49	27.2	1365	10	US-09-968-362-21	Sequence 21, Appl
43	49	27.2	1368	10	US-09-968-362-17	Sequence 17, Appl
44	49	27.2	1371	10	US-09-968-362-19	Sequence 19, Appl
45	49	27.2	1498	12	US-10-447-315-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-009-792A-26
; Sequence 26, Application US/10009792A
; Publication No. US20030153049A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; APPLICANT: JESUNG, Ki-Jun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; FILE REFERENCE: HYLE60.001APC
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-792A-26

Query Match 100.0%; Score 180; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.2e-53;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTTAACTTTAAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGATATCAGC 60
Db 1 ATGTTTAACTTTAAAAGAAATCTTAGTGGGATTAACGGCAGCTTTCATGATATCAGC 60
QY 61 ATGTTTCTGCAACCCCTCTGCAGTGGCCCGCACCATCACCATCACCATATCGAGGA 120
Db 61 ATGTTTCTGCAACCCCTCTGCAGTGGCCCGCACCATCACCATCACCATATCGAGGA 120
QY 121 AGGACTCCGTTAGTCCAGCCAGCTCCCTGCCCGCAGAGCTTCTGCTCAAGTGTAGAG 180

Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 4 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 63
Qy 61 ATGTTTCTGCAACCGCTCTGAGCTGGCCGACCATCACCATCACCATATCGAGGG 119
Db 64 TTGTTTTCGCAACCGCTCTGAGCTGGCCGACCATCACCATCACCATATCGAGGG 122

RESULT 4
US-10-237-386-11
; Sequence 11, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: B. subtilis xylanase sequence with added restriction site
US-10-237-386-11

Query Match 40.4%; Score 72.8; DB 15; Length 657;
Best Local Similarity 91.7%; Pred. No. 3.2e-15;
Matches 77; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 4 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 63
Qy 61 ATGTTTCTGCAACCGCTCTGCA 84
Db 64 TTGTTTTCGCAACCGCTCTGCA 87

RESULT 5
US-10-083-446-177
; Sequence 177, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; USING MULTIVARIANT (IL-3) Hematopoiesis Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
; Corporate Patent Dept., Mail Zone 04E

Db 121 AGGACTCCGTTAGTTCACCGAGCTCCCTGCCCGACAGCTTCTGCTCAAGTGTAGAG 180
RESULT 2
US-10-009-792A-24
; Sequence 24, Application US/10009792A
; Publication No. US20030153049A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; APPLICANT: JEONG, Ki-Jun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; FILE REFERENCE: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-792A-24

Query Match 47.8%; Score 86; DB 15; Length 135;
Best Local Similarity 77.6%; Pred. No. 3.1e-20;
Matches 135; Conservative 0; Mismatches 0; Indels 39; Gaps 1;
Qy 1 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 1 ATGTTTAAGTTTAAAAAGAAATTTCTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Qy 61 ATGTTTCTGCAACCGCTCTGAGCTGGCCGACCATCACCATCACCATATCGAGGGA 120
Db 61 ATGTTTCTGCAACCGCTCTGCA-----84

Qy 121 AGGACTCCGTTAGTTCACCGAGCTCCCTGCCCGACAGCTTCTGCTCAAGTGC 174
Db 85 ---ACTCCGTTAGTTCACCGAGCTCCCTGCCCGACAGCTTCTGCTCAAGTGC 135
RESULT 3
US-10-237-386-10
; Sequence 10, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-10-237-386-10

Query Match 43.9%; Score 79; DB 15; Length 645;
Best Local Similarity 79.0%; Pred. No. 2e-17;
US-10-237-386-10

STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 177:
US-10-083-446-177

Query Match 28.1%; Score 50.6; DB 15; Length 546;
Best Local Similarity 93.0%; Pred.No. 2.4e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGGTTAGGTCACGCACGCTCCTCGCCCCACAGACTTCTGTCTCAAGTGCTTAGAG 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 ACACCATTAGGCTGCCAGCTCCTCGCCCCACAGACTTCTGTCTCAAGTGCTTAGAG 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-10-083-446-178
; Sequence 178, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olin, Peter O.
; Parks, Kuman W.
; Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.2.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-FEB-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-10-083-446-178

Query Match 28.1%; Score 50.6; DB 15; Length
Best Local Similarity 93.0%; Pred. No. 2.4e-07;
Matches 53; Conservative 0; Mismatches 4; Indels

QY 124 ACTCGTTAGGTCACGACGAGTCCTGCCCCAGAGCTTCCTGCTCA
DB 7 ACACCATAGGACCTGCCAGCTCCTGCCCCAGAGCTTCCTGCTCA

RESULT 7
US-10-083-446-53
Sequence 53, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Ceparon, Mairé H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumhan
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of
Using Multivariant (IL-3) Hematopoietic Stem Cells
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation,
Corporate Patent Dept., Mail Zone 0800,
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.2.25

```

DB 7 ACACCAATTAGGACTCCCTGCCCGCCAGACTTCTGCTCAAGTGCTTAGAG 63

RESULT 7
US-10-083-446-53
; Sequence 53, Application US/10083446
; Publication No. US2003018590A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mairé H.
Easton, Alan M. A.
Klein, Barbara K.
McKearn, John P.
Ollins, Peter O.
Paik, Kumnan
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 900 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/083,446
;; FILING DATE: 09-DEC-1996
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/762,227
;; FILING DATE: 09-DEC-1996
;; APPLICATION NUMBER: US 08/192,325
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: US 08/446,872
;; FILING DATE: 06-JUN-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: S. Christopher Bauer
;; REGISTRATION NUMBER: 42,305
;; REFERENCE/DOCKET NUMBER: C-2790/6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (636)737-6257
;; TELEFAX: (636)737-5452
;;
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: nucleic acid
;; LENGTH: 906 base pairs
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-083-446-53

Query Match 28.1%; Score 50.6; DB 15; Length 906;
Best Local Similarity 93.0%; Pred. No. 38-07; 4; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGGTCAGCCAGCTCCCTGCCCGAGAGCTTCCTCTCAAGTGCTTAGAG 180
|||
DB 400 ACACCATTAGGCCCTCCAGCTCCCTGCCCGAGAGCTTCCTCTCAAGTGCTTAGAG 456
|||

RESULT 8
US-10-083-446-72
; Sequence 72, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Bradford-Goldberg, Sarah R.
; Caparon, Mair H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olin, Peter O.
; Palk, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
; Corporate Patent Dept., Mail Zone 04E
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,446
; FILING DATE: 09-DEC-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

;;
;; APPLICATION NUMBER: 08/762,227
;; FILING DATE: 09-DEC-1996
;; APPLICATION NUMBER: US 08/192,325
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: US 08/446,872
;; FILING DATE: 06-JUN-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: S. Christopher Bauer
;; REGISTRATION NUMBER: 42,305
;; REFERENCE/DOCKET NUMBER: C-2790/6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (636)737-6257
;; TELEFAX: (636)737-5452
;;
;; INFORMATION FOR SEQ ID NO: 72:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 921 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-083-446-72

Query Match 28.1%; Score 50.6; DB 15; Length 921;
Best Local Similarity 93.0%; Pred. No. 31e-07; 4; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGGTCAGCCAGCTCCCTGCCCGAGAGCTTCCTCTCAAGTGCTTAGAG 180
|||
DB 7 ACACCATTAGGCCCTCCAGCTCCCTGCCCGAGAGCTTCCTCTCAAGTGCTTAGAG 63
|||

RESULT 9
US-10-083-446-75
; Sequence 75, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Bradford-Goldberg, Sarah R.
; Caparon, Mair H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olin, Peter O.
; Palk, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
; Corporate Patent Dept., Mail Zone 04E
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,446
; FILING DATE: 09-DEC-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/762,227
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 08/446,872

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-083-446-75

Query Match 28.1%; Score 50.6; DB 15; Length 921;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 180
DB 7 ACACATTAGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 63

RESULT 10

US-10-083-446-78
Sequence 78, Application US/10083446
Publication No. US20030185790A1

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

Bauer, S. C.
Braford-Goldberg, Sarah R.
Capaton, Mairé H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olines, Peter O.
Paik, Kuman
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
USING MULTIVARIANT (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E

STREET: 800 N. Lindbergh

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083.446

FILING DATE: 26-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6.

TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 921 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-10-083-446-78

Query Match 28.1%; Score 50.6; DB 15; Length 921;

Best Local Similarity 93.0%; Pred. No. 3.1e-07;

Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 180
DB 7 ACACATTAGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 63

RESULT 11

US-10-083-446-84

Sequence 84, Application US/10083446

Publication No. US20030185790A1

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

Bauer, S. C.

Braford-Goldberg, Sarah R.

Capaton, Mairé H.

Easton, Alan M.

Klein, Barbara K.

McKearn, John P.

Olines, Peter O.

Paik, Kuman

Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
USING MULTIVARIANT (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation

Corporate Patent Dept., Mail Zone 04E

STREET: 800 N. Lindbergh

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (636)737-6257

TELEFAX: (636)737-5452

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-083-446-84

Query Match      28.1%; Score 50.6; DB 15; Length 921;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ATCCGTTAGTCCAGCAGCTCCCTGCCCGCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 ACACCATTAGGCGCTGCCAGCTCCCTGCCCGCAGAGCTTCCTGCTCAAGTGCTTAGAG 456

RESULT 12
US-10-083-446-68
; Sequence 68, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
;   Bauer, S. C.
;   Braford-Goldberg, Sarah R.
;   Caparon, Mairé H.
;   Easton, Alan M.
;   Klein, Barbara K.
;   McKearn, John P.
;   Ollins, Peter O.
;   Paik, Kumnan
;   Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: S. Christopher Bauer, Pharmacia Corporation
          Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-10-083-446-70
Query Match      28.1%; Score 50.6; DB 15; Length 966;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGTCCAGCAGCTCCCTGCCCGCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 ACACCATTAGGCGCTGCCAGCTCCCTGCCCGCAGAGCTTCCTGCTCAAGTGCTTAGAG 501

RESULT 13
US-10-083-446-70
; Sequence 70, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
;   Bauer, S. C.
;   Braford-Goldberg, Sarah R.
;   Caparon, Mairé H.
;   Easton, Alan M.
;   Klein, Barbara K.
;   McKearn, John P.
;   Ollins, Peter O.
;   Paik, Kumnan
;   Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: S. Christopher Bauer, Pharmacia Corporation
          Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-10-083-446-70
Query Match      28.1%; Score 50.6; DB 15; Length 966;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
```

```
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-083-446-68

Query Match      28.1%; Score 50.6; DB 15; Length 966;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCCGTTAGTCCAGCAGCTCCCTGCCCGCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 ACACCATTAGGCGCTGCCAGCTCCCTGCCCGCAGAGCTTCCTGCTCAAGTGCTTAGAG 501

RESULT 13
US-10-083-446-70
; Sequence 70, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
;   Bauer, S. C.
;   Braford-Goldberg, Sarah R.
;   Caparon, Mairé H.
;   Easton, Alan M.
;   Klein, Barbara K.
;   McKearn, John P.
;   Ollins, Peter O.
;   Paik, Kumnan
;   Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: S. Christopher Bauer, Pharmacia Corporation
          Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-10-083-446-70
Query Match      28.1%; Score 50.6; DB 15; Length 966;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
```


Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 180
|||
Db 445 ACACCATAGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 501

RESULT 14

US-10-083-446-71
; Sequence 71, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maitre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olin, Peter O.
Paik, Kuman
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation

Corporate Patent Dept., Mail Zone 04E

STREET: 800 N. Lindbergh

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (636)737-6257

TELEFAX: (636)737-5452

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 966 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 71:

US-10-083-446-71

Query Match 28.1%; Score 50.6; DB 15; Length 966;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 180
|||
Db 445 ACACCATAGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 501

RESULT 15
US-10-083-446-73
; Sequence 73, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maitre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olin, Peter O.
Paik, Kuman
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation

Corporate Patent Dept., Mail Zone 04E

STREET: 800 N. Lindbergh

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (636)737-6257

TELEFAX: (636)737-5452

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 966 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 73:

US-10-083-446-73

Query Match 28.1%; Score 50.6; DB 15; Length 966;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 124 ACTCGTTAGTCCAGCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 180
|||
Db 7 ACACCATAGGCCCTGCCAGCTCCCTGCCAGAGCTTCCTGCTCAAGTGTAGAG 63

Search completed: October 9, 2004, 06:22:17
Job time: 154.651 secs

This Page Blank (uspto)